

**FIGURE 1**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGACTGGCCTCACAACTGCTGTTTCTT  
CTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAAGAGGAAGGGGCAAGGGCG  
GCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACCTGGTGTACGGATGAAACCGTATGCCC  
GCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAG  
AGAAAGTGTGAGGTCAACTTGCAGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCAT  
CAACCACGACCCAGCCGTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACC  
CCTTCACCATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCCCTGTGCGCCGCCGC  
CTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCTG  
CACCTGCATCTTCTTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGACCATCCTCCTTGACCTTT  
GTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

FIGURE 2

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYERNIEEMVA  
QLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGCVNPFTMQEDRSMVSV  
VFSQVPVRRRLCPPPRTGPCRQRAVMETI AVGCTCIF

**FIGURE 3**

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCC  
TGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCACAGTCAC  
GGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGG  
TGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGC  
ACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC  
CAGCGCTCCATCTCACCCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTT  
CGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGC  
GGCTGCTCCAGAGCCTGCTGGTGTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACCT  
GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGCGCTGCACCTGCGTGCTGCCCCGTTTCACT  
GTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCCTATTTATGTG  
TATTTATTGTTATTTATATGCCTCCCCAACACTACCCCTGGGGTCTGGGCATTCCCCGTGTCTGGAGGAC  
AGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGC  
CCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCTGCTCCCGGCTTCCCT  
TACCCTATCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTA  
ACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

FIGURE 4

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLE  
AASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKLAFAECLCRGCIDARTGRE  
TAALNSVRLQLSLLVLRRLRRRPCRDRGSGGLPTPGAFHTEFIHVPVGCTCVLPRSV

Signal peptide:	Amino acids 1-18
Tyrosine kinase phosphorylation site:	Amino acids 112-121
N-myristoylation sites:	Amino acids 32-38;55-61;133-139
Leucine zipper pattern:	Amino acids 3-25
Homologous region to IL-17:	Amino acids 99-195

**FIGURE 5**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGTCAGTCA  
GTGCCCCGACTTGTGACTGAGTGTGCAGTGCCCGAGCATGTACCAGGTCAGTGCAGAGGGCTGCCTGAGGGCT  
GTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGCTGCCAGGTTTGGGGCTGG  
GGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGATGAGGGAGCGACCCAGATTAGGTGA  
GGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCATTCTTGGCAATGGTCATGGGAACCCACACCT  
ACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT  
GTGCCTGTGCCTCCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGA  
CCCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGA  
CCTGTACCACGCCCCGTTGCCTGTGCCCCGACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGG  
GCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACC  
CACAAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGTGT  
GATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACAACCACTTG  
CCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCGTGAAGTGCTGTCTGGAGCAGCAGGATCCCCGGGAC  
AGGATGGGGGGCTTTGGGGAAAACCTGCACTTCTGCACATTTTGAAAAGAGCAGCTGCTGCTTAGGGCCGC  
CGGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAAAGTTCTGCCCATTTCTGGAGGCCACCA  
CTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTGGCCCAGCACAGGCACTTCTAGATATTTCCCC  
CTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATTTGTTTGTGTTTACTCATCACTCAGTGAGCATCTACTTTGG  
GTGCATTCTAGTGTAGTTACTAGTCTTTTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATA  
GAGATTTATCCAAATAAATATCTTTATTTAAAAATGAAAAA

FIGURE 6

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPKSGQDTSEELLRWSTVPVPPLEPARPNRHP  
ESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSELLYHNQTVFYR  
RPCHGEKGTGTHKGYCLERRLYRVSLACVCVRPRVMG

Signal peptide:	Amino acids 1-32
N-glycosylation site:	Amino acids 136-140
Tyrosine kinase phosphorylation site:	Amino acids 127-135
N-myristoylation sites:	Amino acids 44-50;150-156

**FIGURE 7**

ATGCTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCAGGGCGGGCAGGCG  
CCCCGCGCGGCCGCGGGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGG  
CCGGCGTGCTCAGTGCCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCGAGCTGC  
CCGGCAGGGGGCAGGCCCCGGCGACCGCCGCTTCCGGCCGCCACCAACCTGCGCAGCGTGTGCCCCTGGGC  
CTACAGAATCTCCTACGACCCGGCGAGGTACCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCT  
GCCTGACCGGGCTGTTCCGGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCGTGTCTACATGCCACCGTCGTC  
CTGCGCCGCACCCCCGCCTGCGCCGGCGGGCCGTTCGTCTACACCGAGGCCTACGTCACCATCCCCGTGGG  
CTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCCA  
AGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCCTGAGGCCGGTCTGCCCCGGGAGGTCTCCCCGG  
CCCGCATCCCGAGGCGCCCAAGCTGGAGCCGCGCTGGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGCACC  
GAGCAAACCAAGTGCCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGG  
GCATCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACCCGGCACGG  
GCATCCTGTGTGCGGCCCGCATGGAGGGTTTGAAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATC  
GGCTGCTGCGGGTGCAGGGCGTGA CTACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTTTT  
AAAGCAATCTAAAAATAATAATAAGTATAGCGACTATATACCTACTTTTAAATCAACTGTTTTGAATAGA  
GGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTT  
ACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTTGTAGCTGGTACACTCTGG  
CCTGGGTCTCTGAATTCAGCCTGTCAACCGATGGCTGACTGATGAAATGGACACGTCTCATCTGACCCACTC  
TTCCTTCCACTGAAGGTCTTCACGGGCCCTCCAGGTGGACCAAAGGGATGCACAGGCGGCTCGCATGCCCCA  
GGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACCTCGC  
ACAATTTTTTCCCCCTTTTGAAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGA  
ACGTGACATCTTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCA  
GGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCTGTTTCTGCA  
TTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGTCTCTGAACACAATTATTTGT  
AAAAGTTAGTAGTTCTTTTTTAAATCATTAAAAGAGGCTTGCTGAAGGAT

**FIGURE 8**

MLVAGFLLALPPSWAAGAPRAGRPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASC  
PAGGRP GD RR FR PPTNLR SVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFG EEDVRFRSAPVYMPTVV  
LRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQAKLLLGPNDAPAGP

Signal peptide:	Amino acids 1-15
N-glycosylation sites:	Amino acids 68-72;181-185
Tyrosine kinase phosphorylation site:	Amino acids 97-106
N-myristoylation sites:	Amino acids 17-23;49-55;74-80; 118-124
Amidation site:	Amino acids 21-25

**FIGURE 9**

CAACTGCACCTCGGTTCTATCGATAGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCAT  
GGTCAAGTACTTGCTGCTGTCGATATTGGGGCTTGCCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCA  
AAGTAGGACATACTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGAC  
ATTGGCATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG  
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGAACTTGG  
GCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAAGAGACCCTGGTCGTC  
CGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCTGGTGAAGTGTGGCTGCACCTG  
CGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCCACTCAGCTGAAGAAG

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**FIGURE 10**

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINENQRVSMS  
RNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSVSFQ  
LEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

Amino acids 1-30

N-glycosylation site:

Amino acids 83-86

N-myristoylation sites:

Amino acids 106-111;136-141

**FIGURE 11**

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGT  
TCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGAGACTTGA  
GGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTGCAACAGGGGACTATTCAATTTTGATGAATGTAAGC  
TGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAA  
CTTCCAGTCCTACAGCTGTGTGAGGTGCAATTACACAGAGGCCCTTCCAGACTCAGACCAGACCCTCTGGTG  
GTAAATGGACATTTTCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAAT  
ATTCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTTCACCTCACCAGGCTGCCTAGA  
CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTA  
AGAAGAATGAGGAGACAGTAGAAGTGAACCTTCAACCACTCCCTGGGAAACAGATACATGGCTCTTATC  
CAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGT  
GGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGACGCTGACTCCATATTTTCTACTTGTGGCA  
GCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCCAAACAGGCGTCCCTTTCCCTCTGGATAAC  
AACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT  
GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGC  
CCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAA  
TTTCTTCAAAACCATTGCAGAAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGG  
TCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCA  
ACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCC  
CTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCTATCTGCACAAATACGTGGTGGTCTACTT  
TAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATG  
CCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAGCCTGC  
CACGATGGCTGCTGCTCCTTGTAG

**FIGURE 12**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRLDRVEPVTTTSVATGDYSILMNVS  
WVLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK  
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKQQVSAGKRSQACHD  
GCCSL

Signal sequence:

Amino acids 1-14

Transmembrane domain:

Amino acids 290-309

N-glycosylation sites:

Amino acids 67-70;103-106;156-159;  
183-186;197-200;283-286

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 228-231;319-322

N-myristoylation site:

Amino acids 116-121

Amidation site:

Amino acids 488-491

**FIGURE 13**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGGACAGAG  
AGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCTCTGGAGGCTGAAGAGGGATTCCAGCCCCTGCCA  
CCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCACAGGGCCTCAGGCCTGGGT  
GCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGCTGTCTTGGCACTGGGCGGAAGCCCAGTGG  
TCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTC  
TGGGACAGTGACATACTCTGCCTGCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCA  
CCTGCAGACAGAGCTGGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCC  
ACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGG  
GTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTACTGCCCG  
CTGCGTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATAT  
GACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAAGGA  
ACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGGTGACAACGTGCATC  
TGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCA  
AAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTG  
CCTCTGTATTACAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCCAGGGAGGACC  
CCCGCGCACACCAGAACCTCTGGCAAGCCGCCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCTGGAC  
GCACCGTGCTCGCTGCCCCGAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACT  
GGTCCACCGCTTTCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACC  
CTAACCTCTGTGTTACAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTG  
GGGCCTCTCAAAGACGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTT  
GGAACCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTAC  
TACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCC  
ATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTC  
CCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCGCTCGG  
GGGCGGCCCGCAGGGGCCGCGCGGCTCTGCTCCTTACTCAGCCGATGACTCGGGTTTCGAGCGCCTGGTG  
GGCGCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGACCTGTGGAGCCGTCGTGAACT  
GAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAGCGGCCAGACCCTGCAGGAGGGCGGCGTGGTGG  
TCTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGG  
GCGCACGGCCCGCACGACGCCTTCCGCGCCTCGCTCAGCTGCGTGCTGCCGACTTCTTGACAGGGCCGGG  
GCCCCGACGTACGTGGGGGCTGCTTCGACAGGCTGCTCCACCCGACGCCGTACCCGCCCTTTTCCGCA  
CCGTGCCCCGTCTTCACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCG  
CGTTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCCAGCCAGCCCTGGATAGCTACTT  
CCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGGACGGGA  
CTTAAATAAAGGCAGACGCTGTTTTCTAAAAAA

**FIGURE 14**

MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGPVLAPTHLQTELV  
 LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVLSFQAYPTARCVLLEV  
 QVPAALVQFGQSVGSSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSAADGNVHLVLNV  
 EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ  
 LWQAARLRLTLQSWLLDAPCSLPAEAALCWRAPGGDPCLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ  
 VNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS  
 GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSAAAARG  
 RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFHAQRRQTLQEGGVVLLFSP  
 GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHLPDAVPALFRTVPVFT  
 LPSQLPDLFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPGTPAPGRGVGPGAGPGAGDGT

signal sequence:

Amino acids 1-20

transmembrane domain:

Amino acids 453-473

N-glycosylation sites:

Amino acids 118-121;186-189;198-201;  
 211-214;238-241;248-251;334-337;  
 357-360;391-394

Glycosaminoglycan attachment site: Amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-555

N-myristoylation sites:

Amino acids 107-112;152-157;319-324;  
 438-443;516-521;612-617;692-697;  
 696-701;700-705

**FIGURE 15**

CGAGGGCTCCTGCTGGTACTGTGTTTCGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAGGCCATGCAG  
CCATGTTCCGGGAGCCCTAATTGCACAGAAGCCCATGGGGAGCTCCAGACTGGCAGCCCTGCTCCTGCCTC  
TCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGCTTTCGCCACCTGCCCCACTGGAACACC  
CGCTGTCTCTGGCCTCCACACGGATGACAGTTTCACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTG  
GTGGGCCCTCTTCTCCACAAAGCCTTGGTGTGTGCGAGTCTGGCACTGTTCCCGCTGTTTGTGCCAGCATCTGC  
TGTCAGGTGGCTCAGGTCTTCAACGGGGCCTCTTCCACCTCCTGGTGCAGAAATCCAAAAGTCTTCCACA  
TTCAAGTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTACCTGTCT  
TGAGAAGAGCCATCACATTTCCATCCCCCTCCCCAGACATCTCCACAAGGGACTTCGCTCTAAAAGGACCC  
AACCTTCGGATCCAGAGACATGGGAAAGTCTTCCCAGATTGGACTCACAAAGGCATGGAGGACCCGAGTTC  
TCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTCCGGGTGACCATATCTTCAGGCCCTGAGGTGAGCGTGCG  
TCTTTGTCAACAGTGGGCACTGGAGTGTGAAGAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTG  
GGGGCCACACTGTAGAGCTGCCTTATGAATTCCTTCTGCCCTGTCTGTGCATAGAGGCATCTACCTGCAA  
GAGGACACTGTGAGGCGCAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAA  
GTCAGTGCACCTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCCCACTGA  
AGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATACCCCTTTGCAAAGACCTCCCGAATGCCACGGCT  
CGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCCCAGCTCTGCTTCAAGTTCTCTTT  
TGGAACAGCAGCCATGTTGAATGCCCCCACCAGACTGGGTCTCTCACATCCTGGAATGTAAGCATGGATA  
CCCAAGCCCAGCAGCTGATTCTTCACTTCTCCTCAAGAATGCATGCCACCTTCACTGCTGCCTGGAGCCTC  
CCAGGCTTGGGGCAGGACACTTTGGTGGCCCCCGTGTACACTGTGAGCCAGGCCCGGGGCTCAAGCCCAGT  
GTCACTAGACCTCATCATTTCCCTTCCCTGAGGCCAGGGTGCTGTGTCTGCTGGTGTGGCGGTGAGATGTCCAGT  
TTGCCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCACTGCTG  
GCCCTCCTCACCTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCACAGTCAGGCCCGGGCCAGC  
GCGGCCAGTGCTCCTCCTGCACGCGGCGGACTCGGAGGCGCAGCGCGCCTGGTGGGAGCGCTGGCTGAAC  
TGCTACGGGCAGCGCTGGGCGGCGGGCGGACGTGATCGTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGT  
GGGCCCGCTGCCGTGGCTCTGGGCGGCGGACGCGCGTAGCGGGAGCAGGGCACTGTGCTGCTGCTGT  
GGAGCGGCGCCGACCTTCGCCCCGTGAGCGCCCCGACCCCCGCGCCGCGCCCCCTGCTCGCCCTGCTCCAC  
GCTGCCCCGCGCCCGCTGCTGCTGCTCGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCGCC  
GCTGCGCGCCCTGCCGCGCTACCGCCTGCTGCGCGACCTGCCGCGTCTGCTGCGGGCGCTGGACGCGCGGC  
CTTTGCGAGAGGCCACCAGCTGGGGCCGCTTGGGGCGCGGCAGCGCAGGCAGAGCCGCTAGAGCTGTGC  
AGCCGGCTTGAACGAGAGGCCGCCGACTTGACAGACCTAGGTTGAGCAGAGCTCCACCGCAGTCCCCGGTGTCT

**FIGURE 16**

MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSFSGSSAYIPCRTWWALFSTKPWCV  
RVWHCSRCLCQHLLSGGSLQRGLFHLLVQKSKKSSTFKFYRRHKMPAPAQRKLLPRRHLSEKSHHISIPS  
PDISHKGLRSKRTQPSDPETWESLPRLDSPQRHGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHQWALECE  
ELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQH  
TQMVMALTLCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKFSFGNSSHVECPH  
QTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDLIIPFLR  
PGCCVLVWRSDVQFAWKHLLCPDVSYRHLGLLILALLALLTLLGVVLALTCRRPQSGPGPARPVLLHAAD  
SEAQRRLVGALAEELLRAALGGGRDVIVDLWEGRHVARVGPLPWLWAARTRVAREQGTVLLLWSGADLRPVS  
GPDPRAPLLALLHAAPRPLLLLAYFSRLCAKGDIPPPLRALPRYRLRLDLPRLLRALDARPF AEATSWGR  
LGARQRRQSRLELC SRLEREAA RLADLG

Signal peptide:	Amino acids 1-23
Transmembrane domain:	Amino acids 455-472
N-glycosylation sites:	Amino acids 318-322;347-351;364-368
Glycosaminoglycan attachment site:	Amino acids 482-486
cAMP- and cGMP-dependent protein kinase phosphorylation sites:	Amino acids 104-108;645-649
Tyrosine kinase phosphorylation site:	Amino acids 322-329
N-myristoylation sites:	Amino acids 90-96;358-364;470-476
Eukaryotic cobalamin-binding proteins:	Amino acids 453-462

FIGURE 17

GCCAGGCCCTATCTCCCTGCCAGGAGGCCGGAGTGGGGGAGGTGAGACGGGGCGGTTGGAGGGGGAGGGAT  
GCCACGCGCTTCTGCCTCAGGTGTTCTCGCTTGTTTGTTCAGTGGAGAGCAGGGAGTGGGGCCAGCCAGCA  
GAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAG  
CATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAT  
TCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCGGGTAATACTGGAGGAGCTGAAGT  
CGGAGGGAAGACAGTGCCAACAACCTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAGAAGT  
GGAATGGAATCTCAACCTTTCTGAATATGAAATTTGAAACGGATTATTTTCGTAAAGGTTGTCCCTTTTCC  
TTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGC  
CGGACAATCTAGCTTGTAACCCCTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGC  
AGGTGTCTCTTCGACCACGCACCGCATGGCTCGGACATGCAGGTGTCTTCGACCACGCACCGCACAACTTC  
GGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAGCA  
GGAGCAAACCTACAGAGATGACCAGCTGCCTCCTTCAAATGTTTCTCCAGGGGATTATATAATTGAGCTGG  
TGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCCTCCCGTGGGCCGGG  
CCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGAT  
GTGCCGCAAGAAGCAACAAGAAAATATATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACA  
CTGCAGCACTCCCAAGAGAGAGGCTCCGGCCGCGGCCGAAGGTCTTCTCTGCTATTCCAGTAAAGATGGC  
CAGAATCACATGAATGTCGTCCAGTGTTTCGCCTACTTCCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCT  
GGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAGAATGGGTCTATCCAGAAGATCCACGAGT  
CCCAGTTCATCATTGTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAA  
GGAGGTGGCCGAGGCTCGGGGAAAGGAGAGCTCTTCTGGTGGCGGTGTGAGCCATTGCCGAAAAGCTCCG  
CCAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCTTGCGAGG  
GAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTTCC  
CACCTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGGCAGCAGAAGGAACCTA  
CTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGC  
CCGACTGGTTCGAAAAGCAGTTCGTTCCCTTCCATCCTCCTCCACTGCGCTACCGGGAGCCAGTCTTGAG  
AAATTTGATTTCGGGCTTGTTTTAAATGATGTGATGTGCAAAACCAGGGCCTGAGAGTGACTTCTGCCTAAA  
GGTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCAGCACGAGAGTCAGCATGGGGGCCTGG  
ACCAAGACGGGGAGGCCCGCCTGCCCTTGACGGTAGCGCCGCCCTGCAACCCCTGCTGCACACGGTGAAA  
GCCGGCAGCCCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTC  
TCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGAAACGTCTTCCCTGACGGAGAGCGTGTCTCCT  
CTTCAGGCCTGGGTGAGGAGGAACCTCCTGCCCTTCTTCCAAGCTCCTCTCTTCTGGGTGATGCAAAGCA  
GATCTTGGTTGCCCGAGCTACACTGATGAACTCCACGCGGTGCCCCCTTTGTAACAAAACGAAAGAGTCTA  
AGCATTGCCACTTTAAAAA

**FIGURE 18**

MPRASASGVPA LFVSGEQGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVT  
 ILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF  
 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHGSDMQVSFDHAPHN  
 FGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA  
 GPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKD  
 GQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKH  
 KGGGRGSGKGELFLVAVSAIAEKLQAKQSSSAALSKFIAVYFDYSCEGDVPGILDLS TKYRLMDNLPQLC  
 SHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRS LYVAICNMHQFIDEEDWFEKQFVPFHPPLRYREPVL  
 EKFD SGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGLDQDGEARPALDGSAA LQPLLHTV  
 KAGSPSDMPRDSGIYDSSVPSSLSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPALPSKLLSSGSK  
 ADLGCRSYTDELHAVAPL

Transmembrane domain:

Amino acids 283-307

N-glycosylation sites:

Amino acids 31-34;38-41;56-59;  
113-116;147-150;182-185;266-269

Glycosaminoglycan attachment sites: Amino acids 433-436;689-692

cAMP- and cGMP-dependent protein kinase phosphorylation:

Amino acids 232-235

Tyrosine kinase phosphorylation sites: Amino acids 312-319;416-424

N-myristoylation site:

Amino acids 19-24;375-380;428-433;  
429-434;432-437;517-522;574-579;  
652-657;707-712



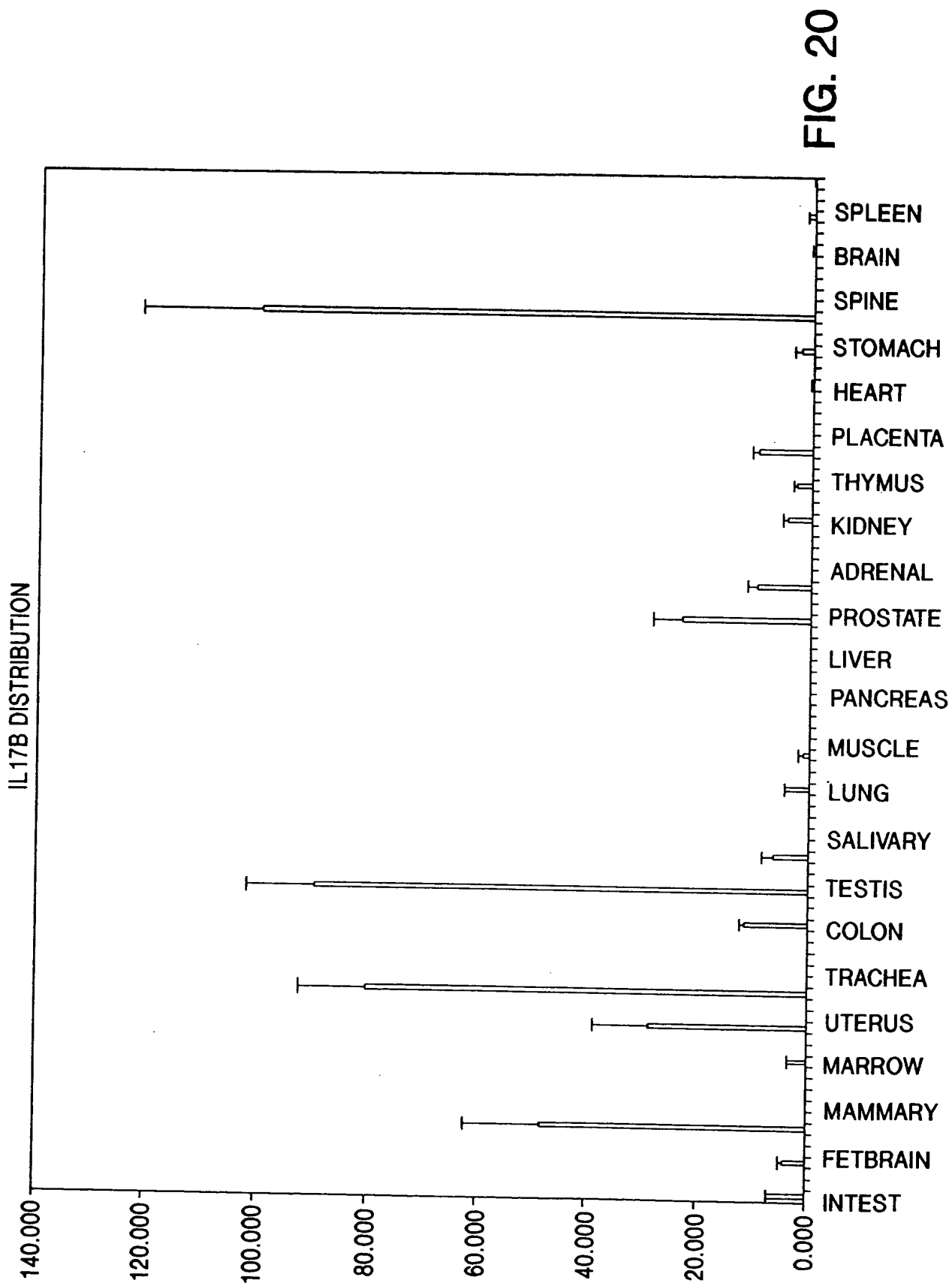


FIG. 20

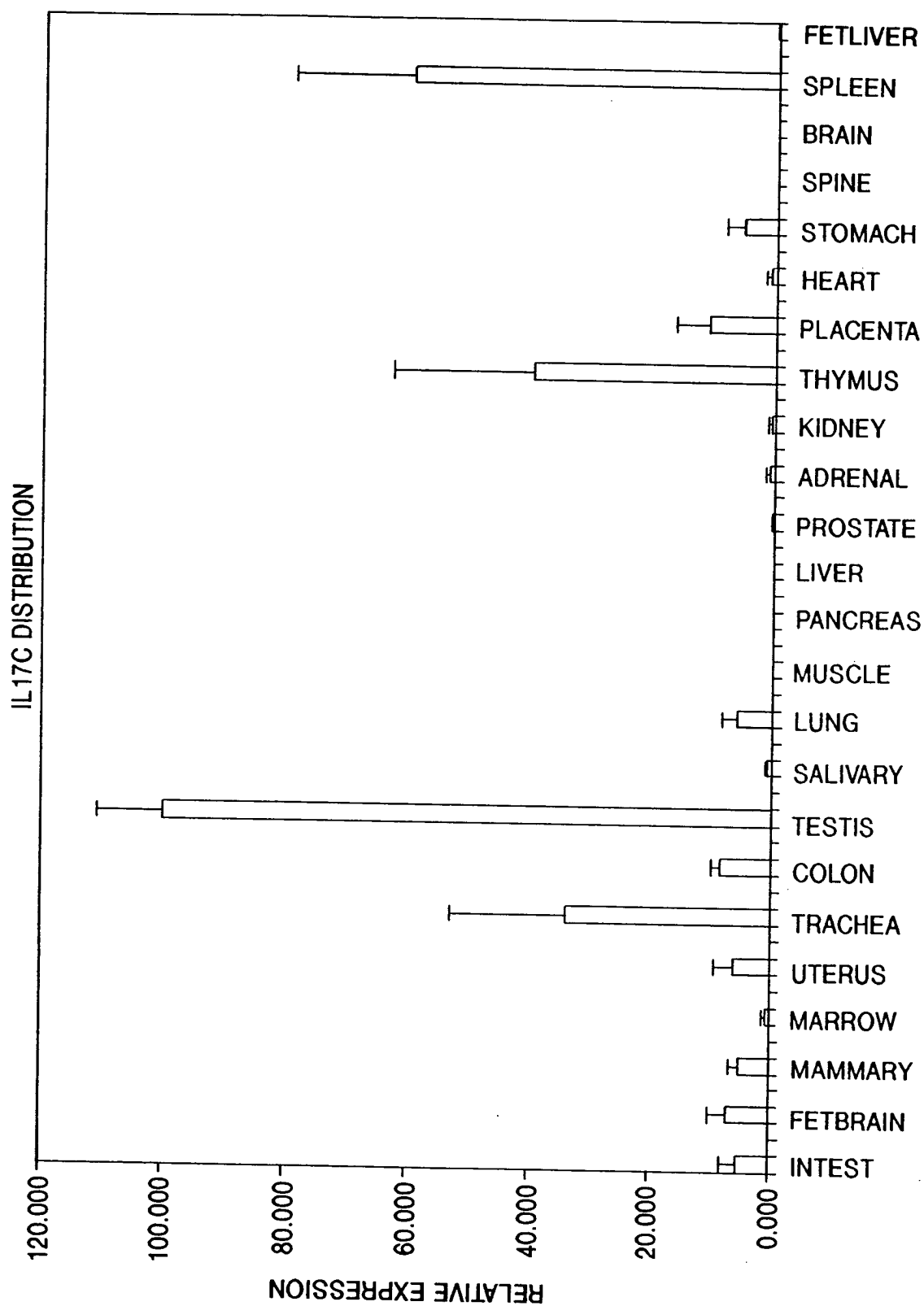
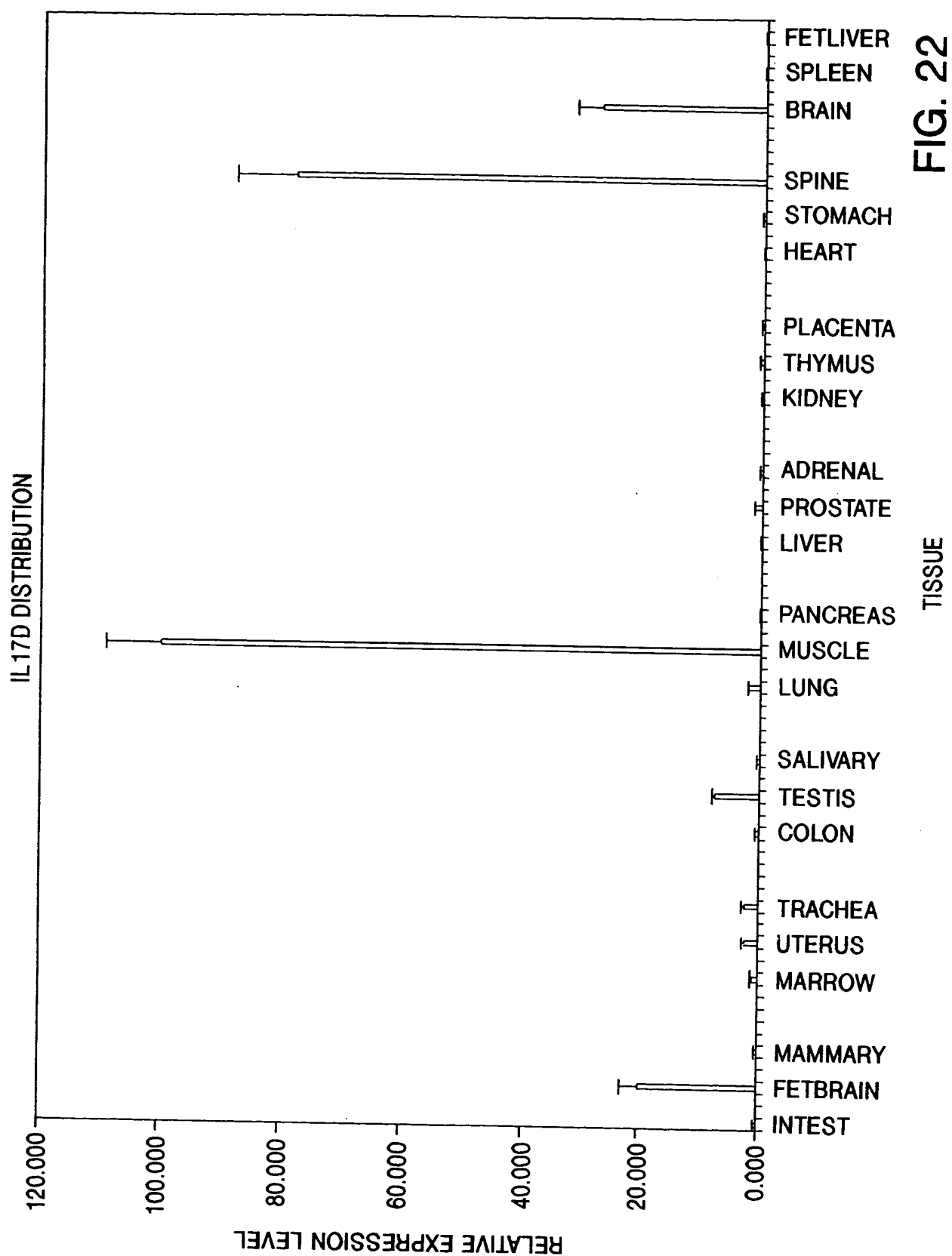


FIG. 21



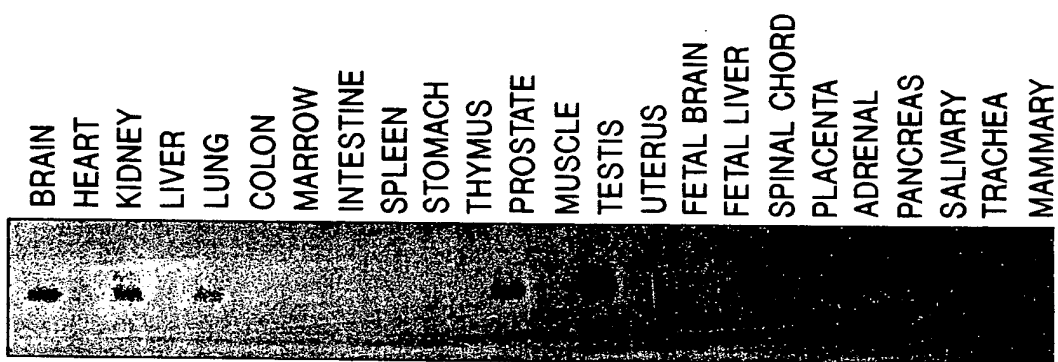


FIG. 23

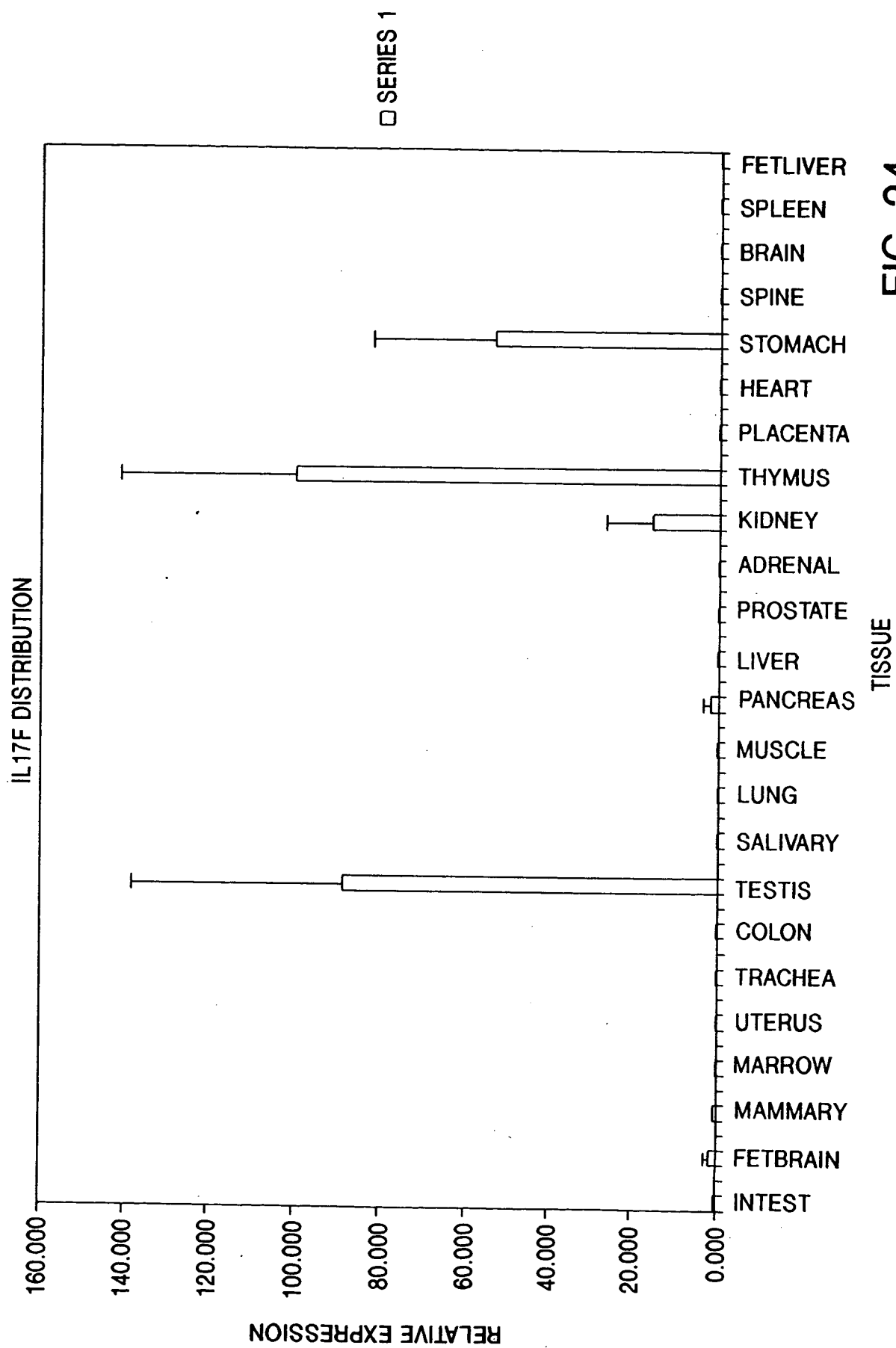


FIG. 24

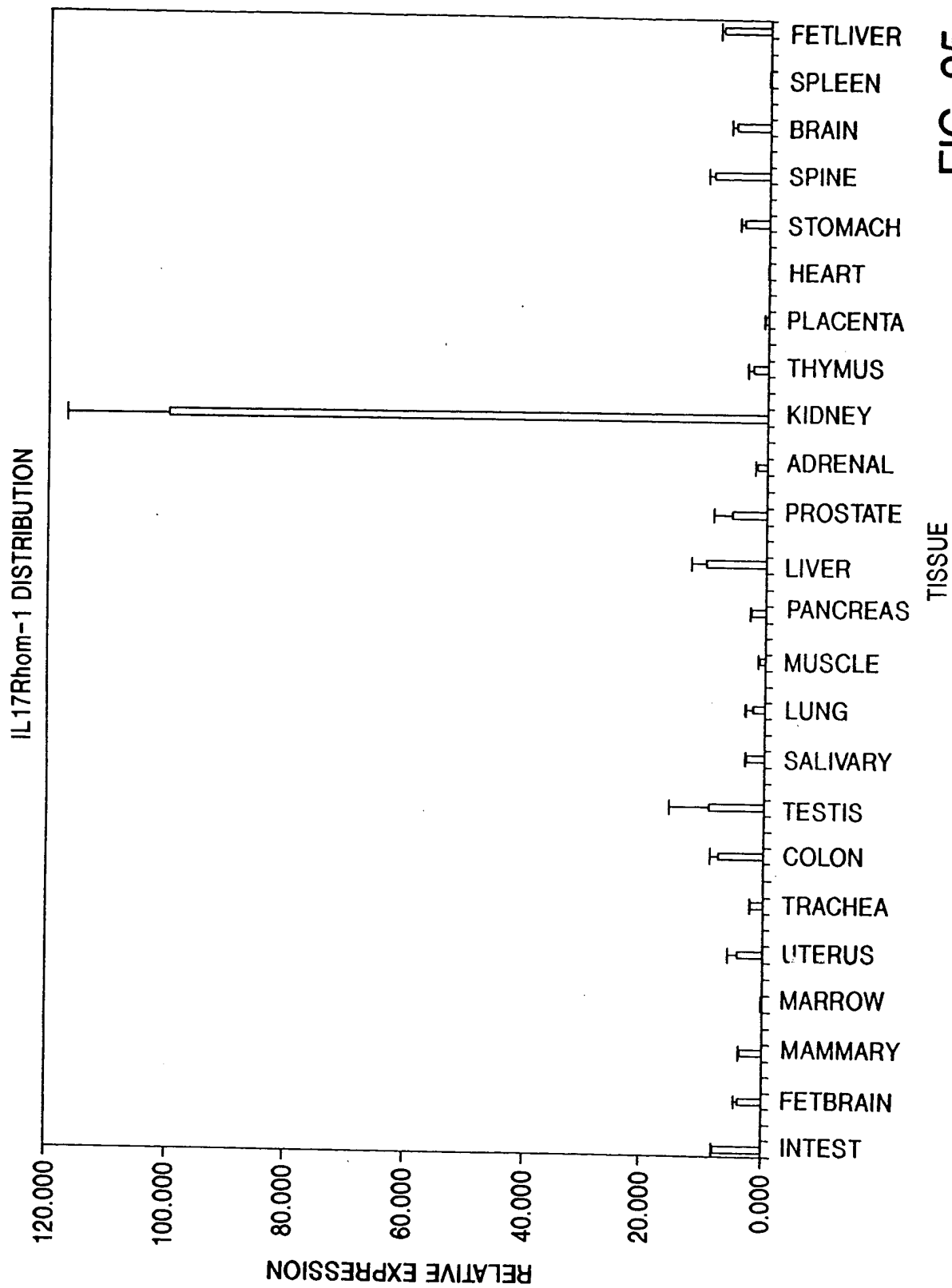


FIG. 25

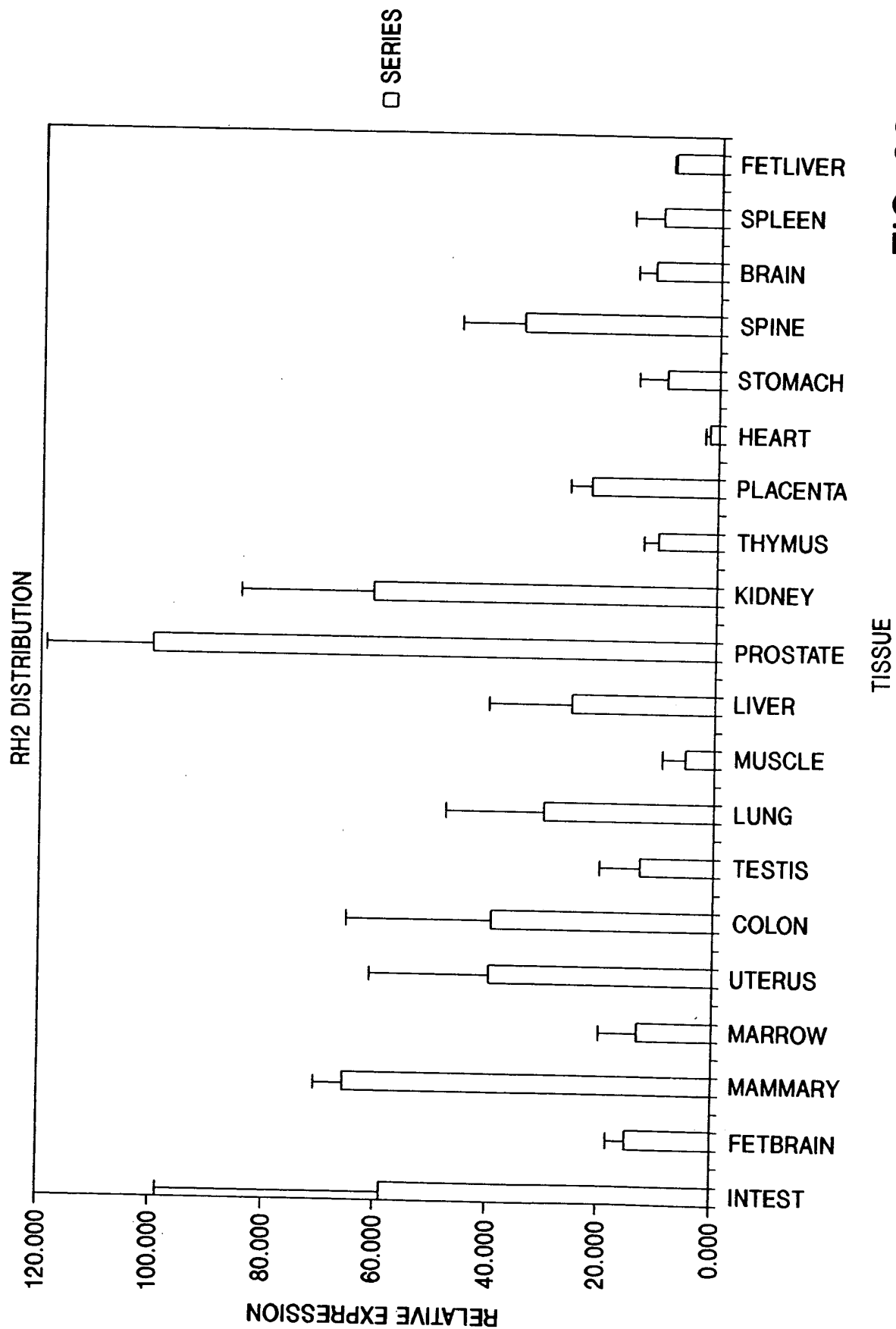


FIG. 26

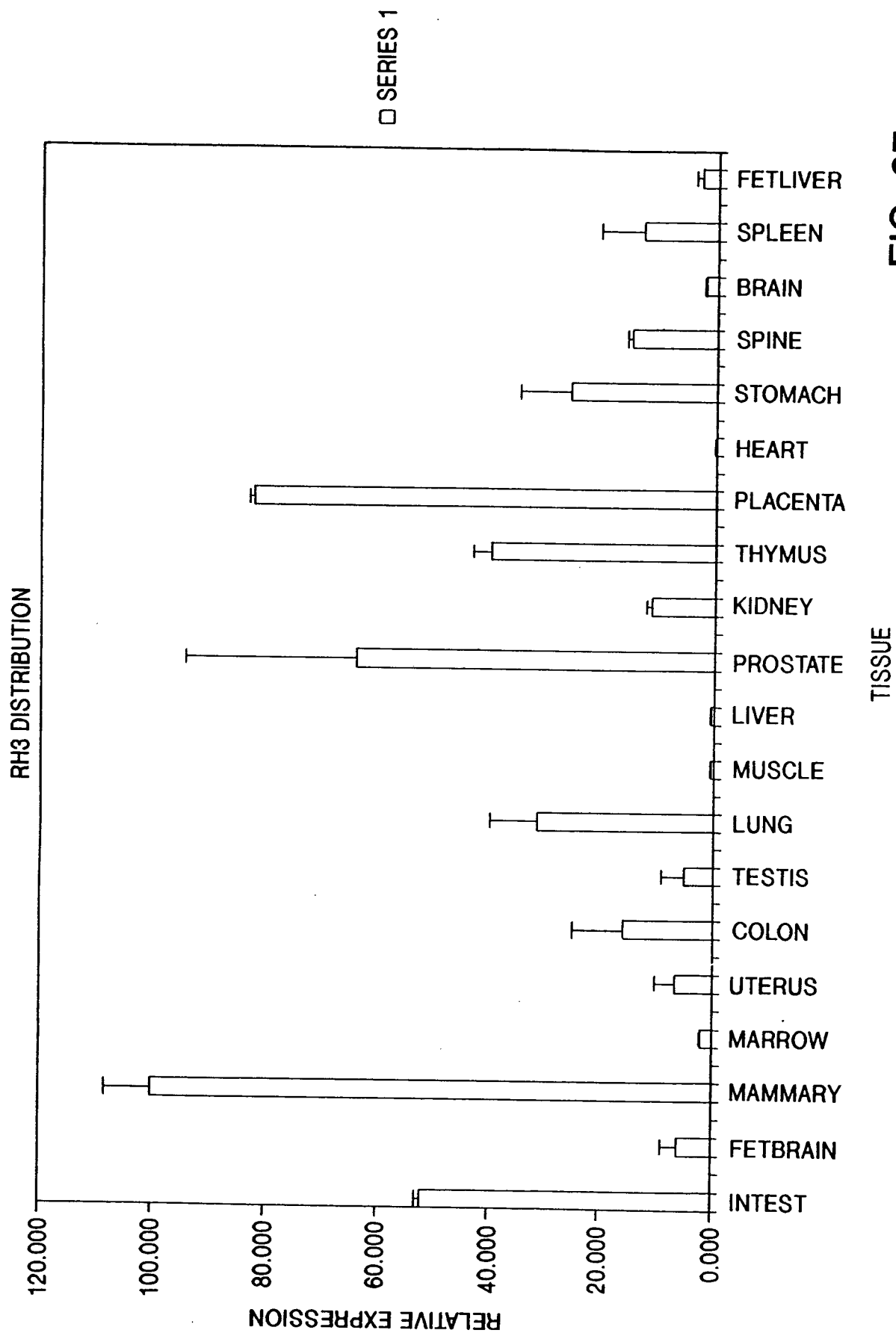


FIG. 27

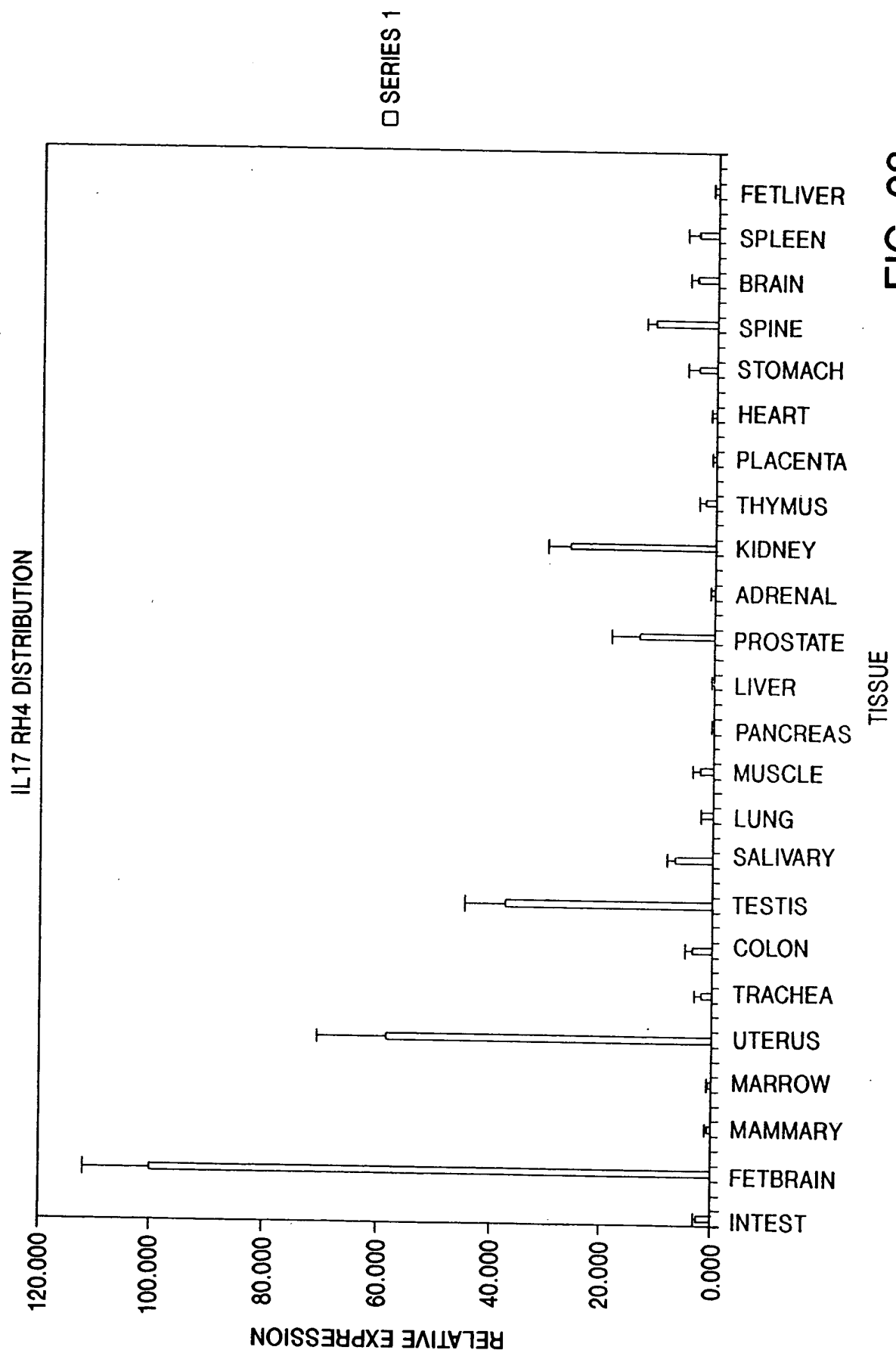


FIG. 28

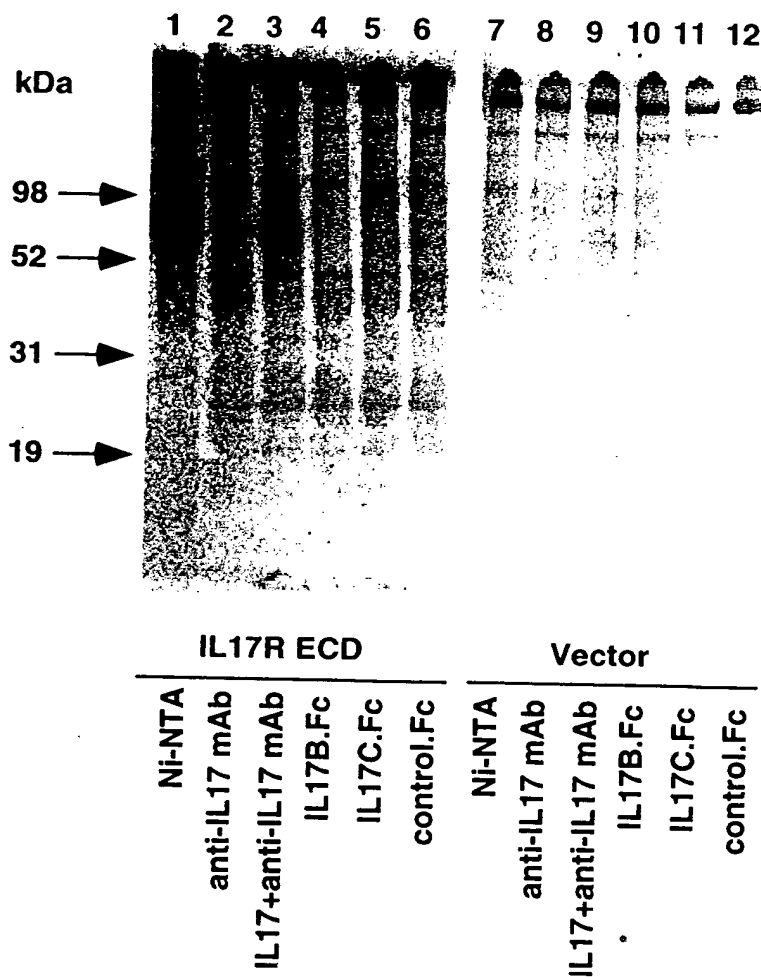


FIG. 29A

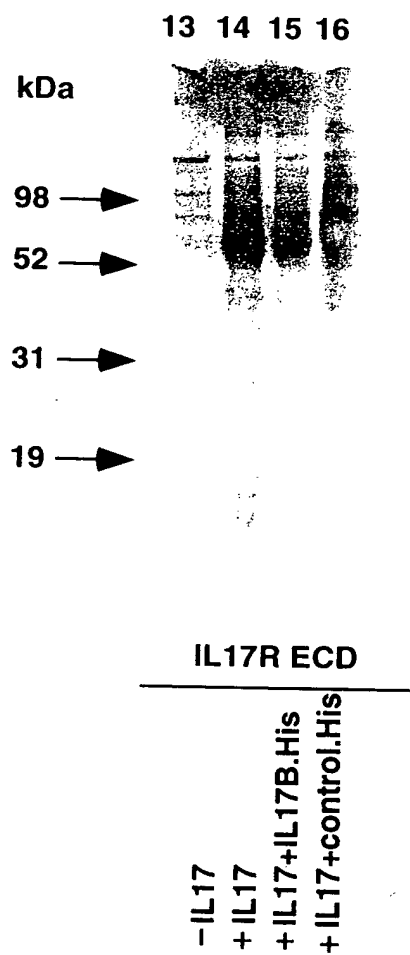


FIG. 29B



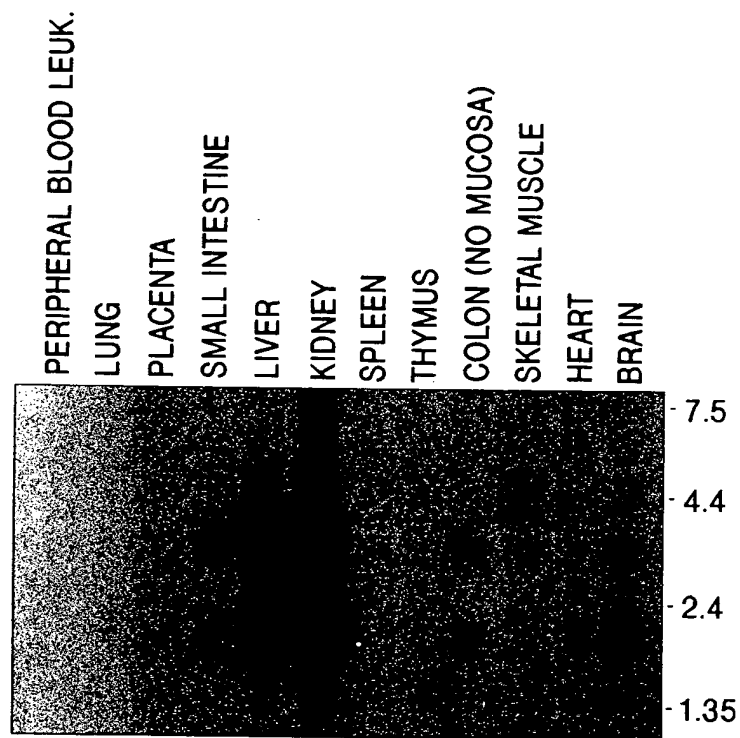


FIG. 31A

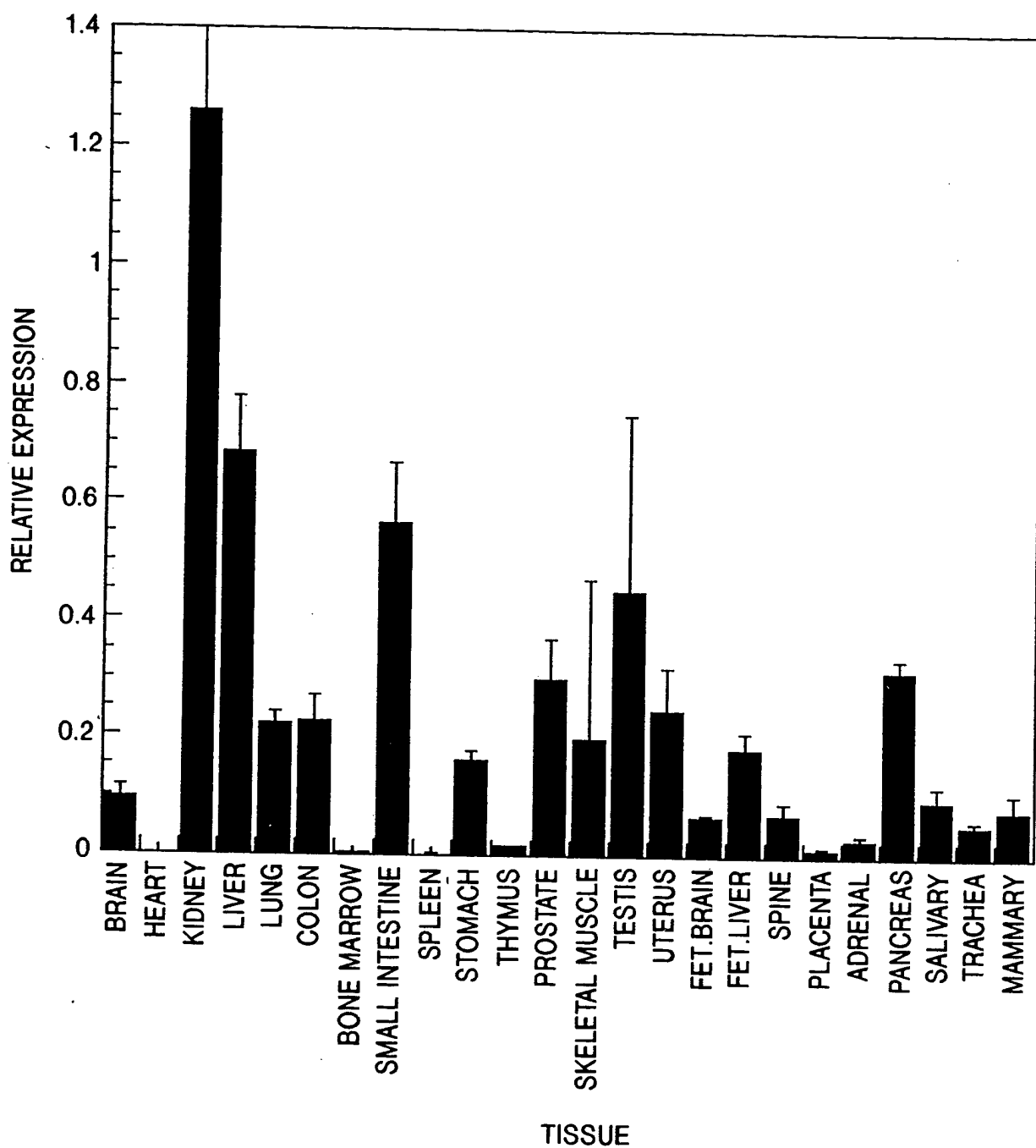


FIG. 31B

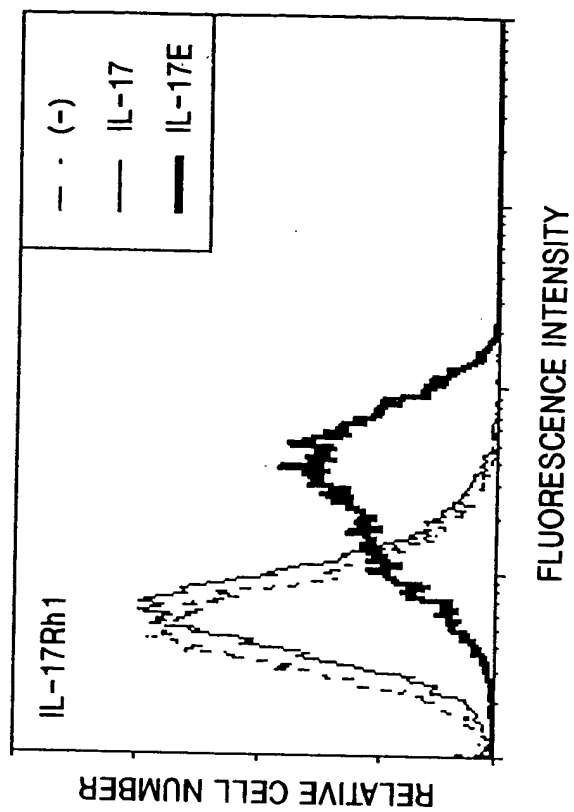
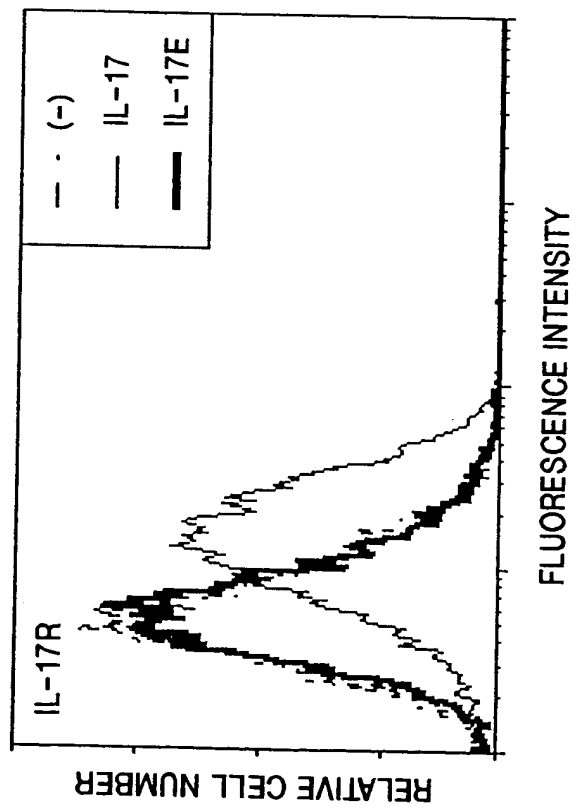


FIG. 32A

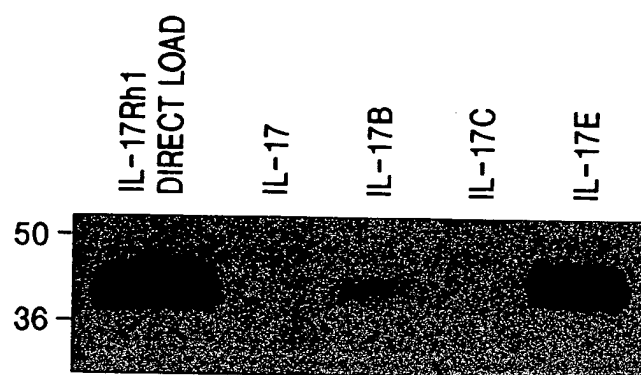
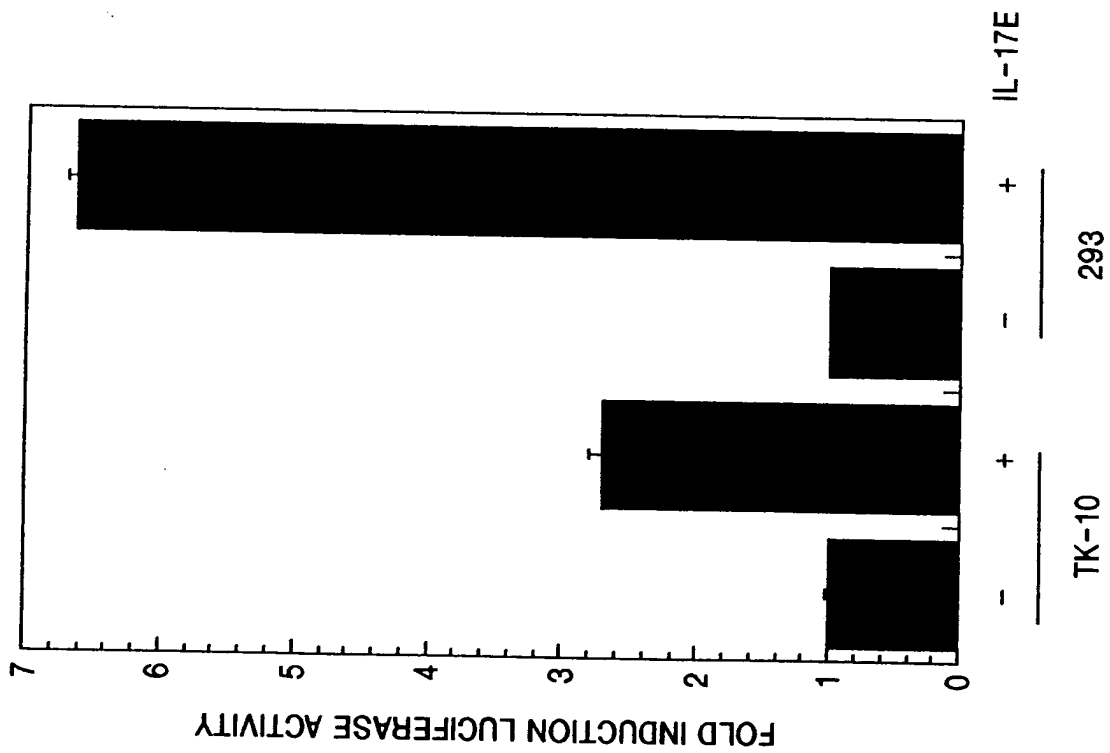
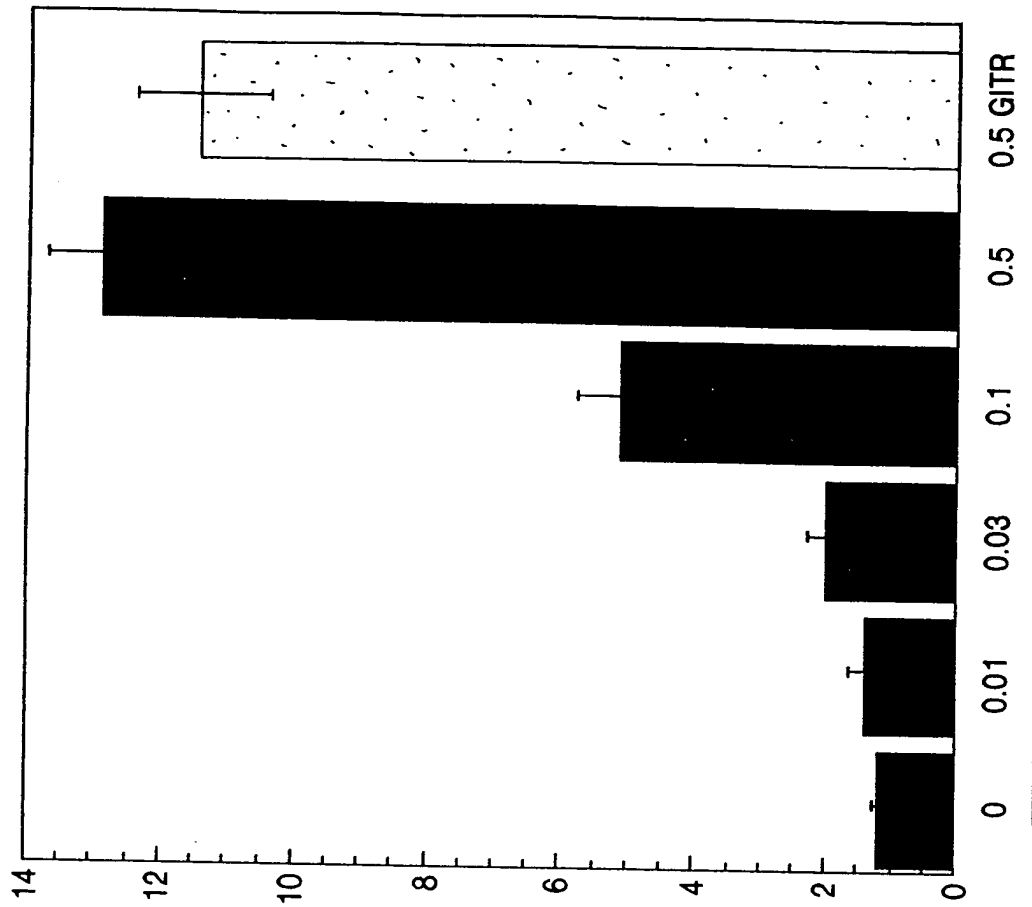


FIG. 32B



TK-10 293

FIG. 33A



IL-17E EXPRESSION VECTOR (µg)

FIG. 33B

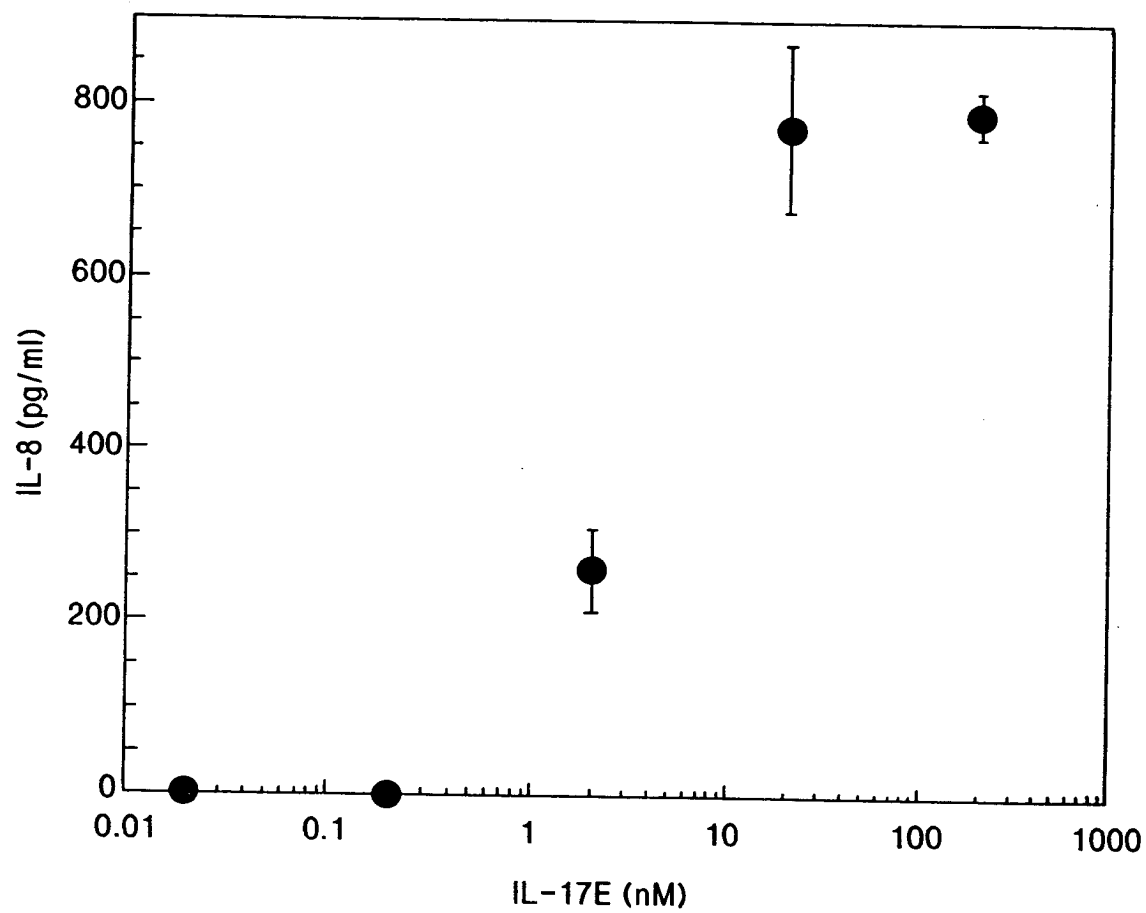


FIG. 34

IL-17 FAMILY OF CYTOKINES HAS COMPLEX PATTERN  
OF OVERLAPPING RECEPTOR-LIGAND SPECIFICITIES

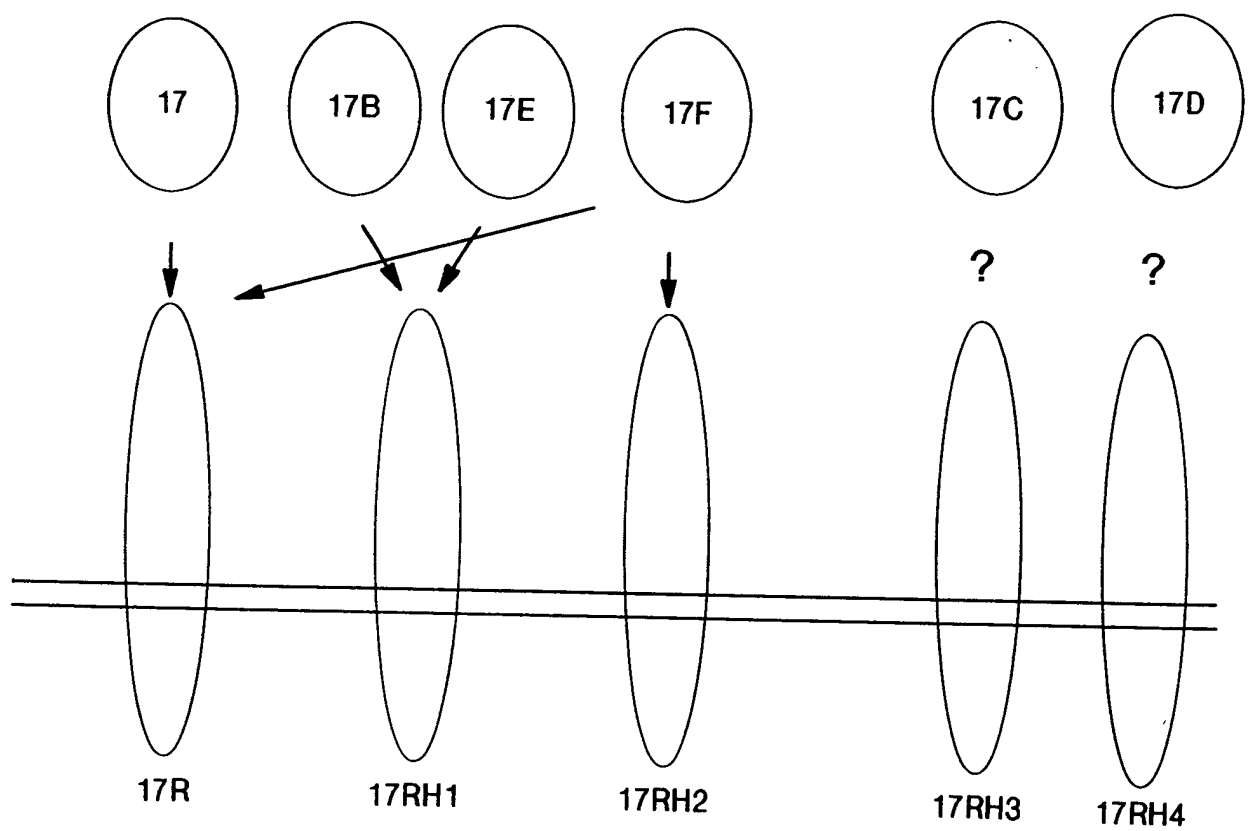


FIG. 35

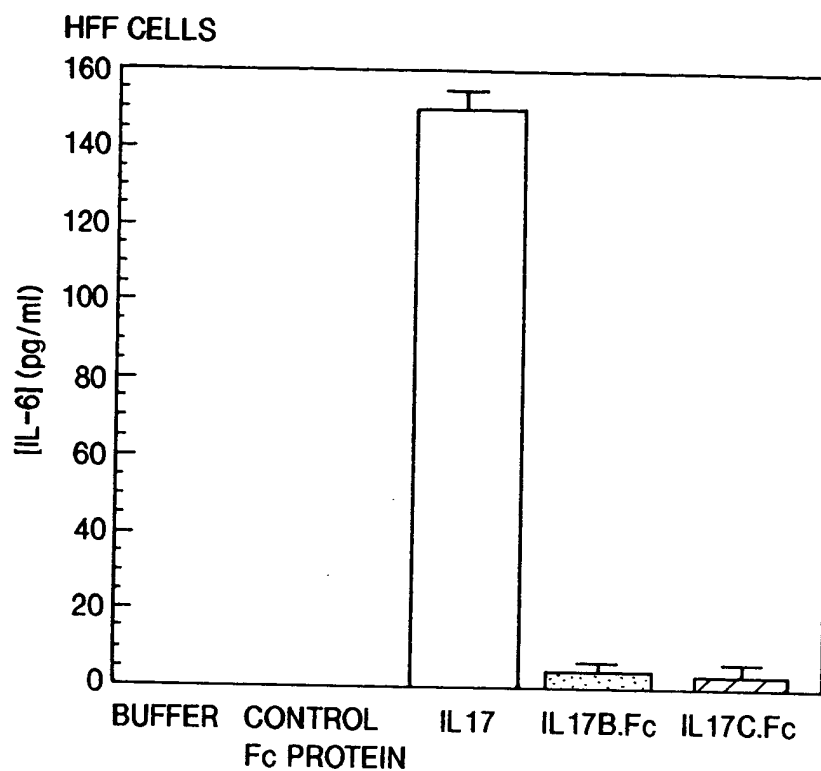


FIG. 36A

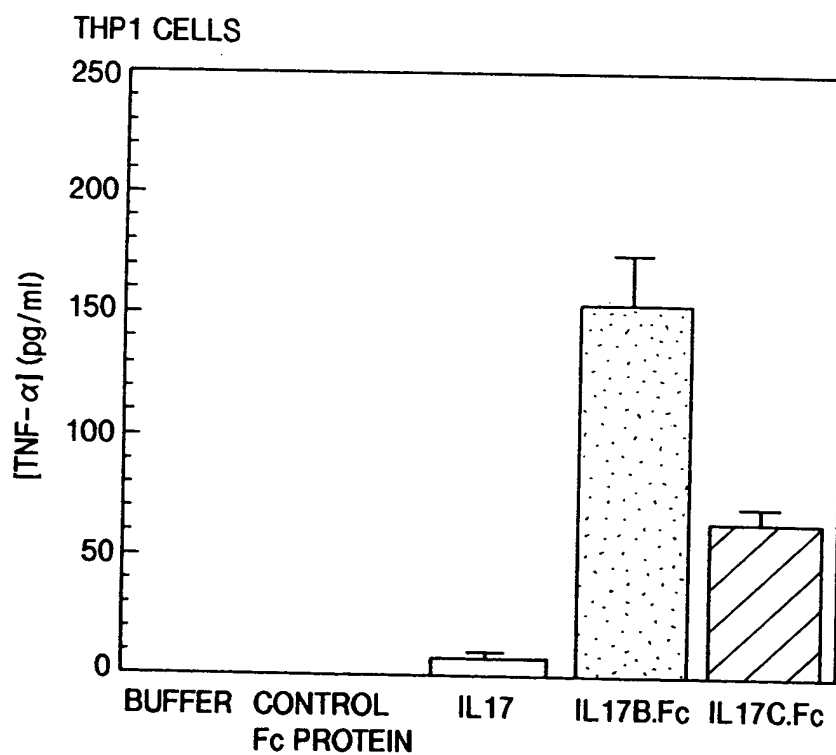


FIG. 36B

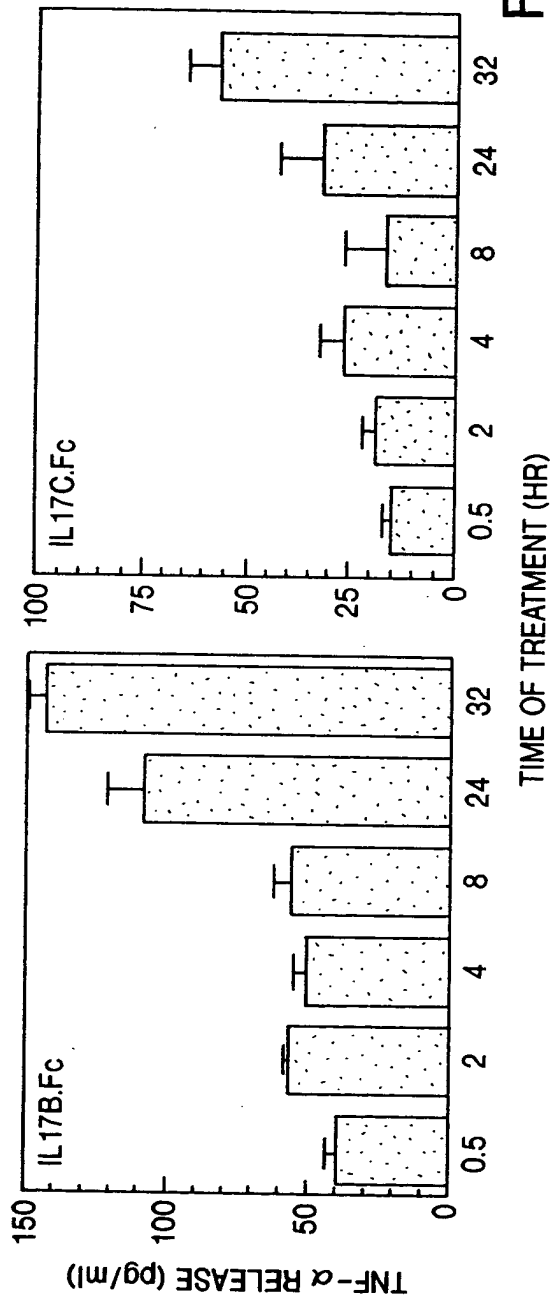


FIG. 37A

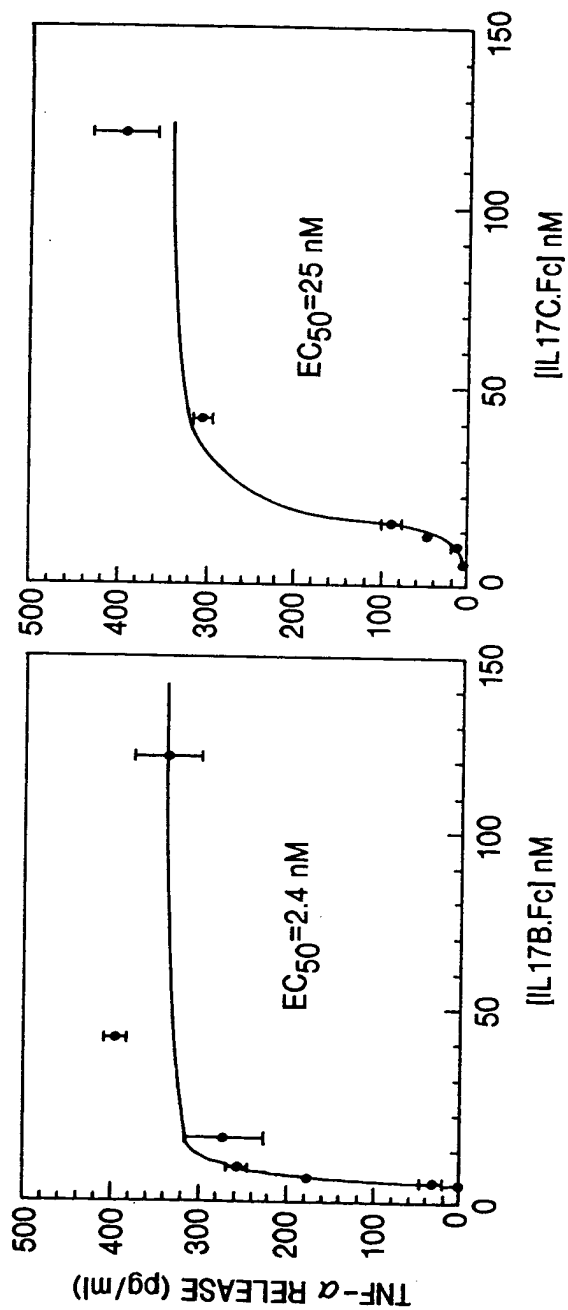


FIG. 37B

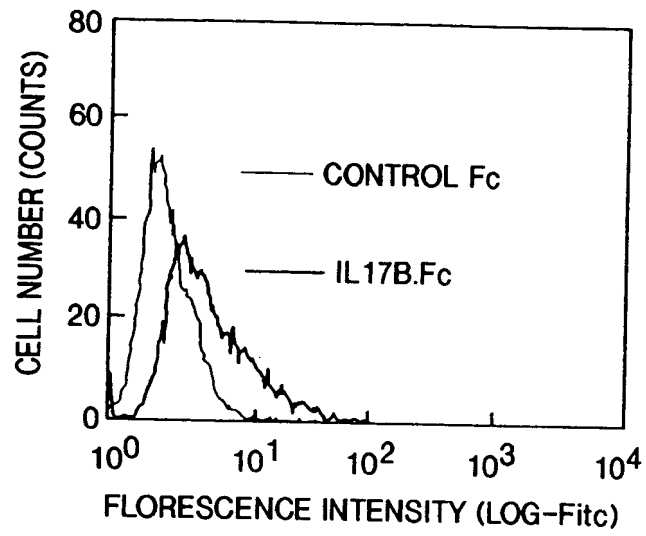


FIG. 38A

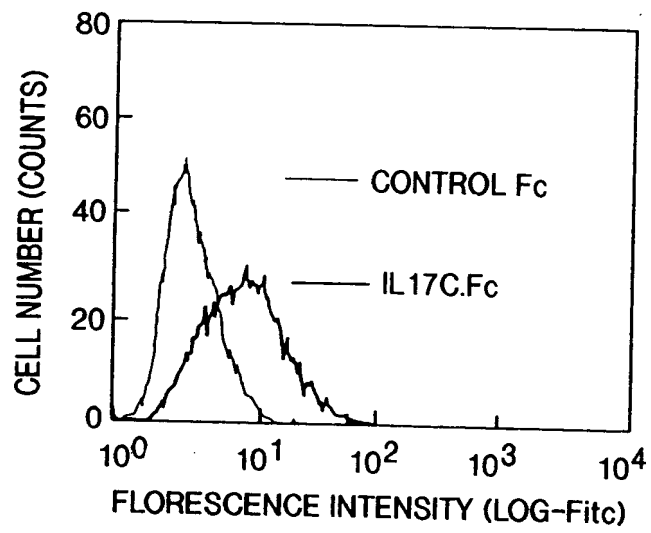


FIG. 38B

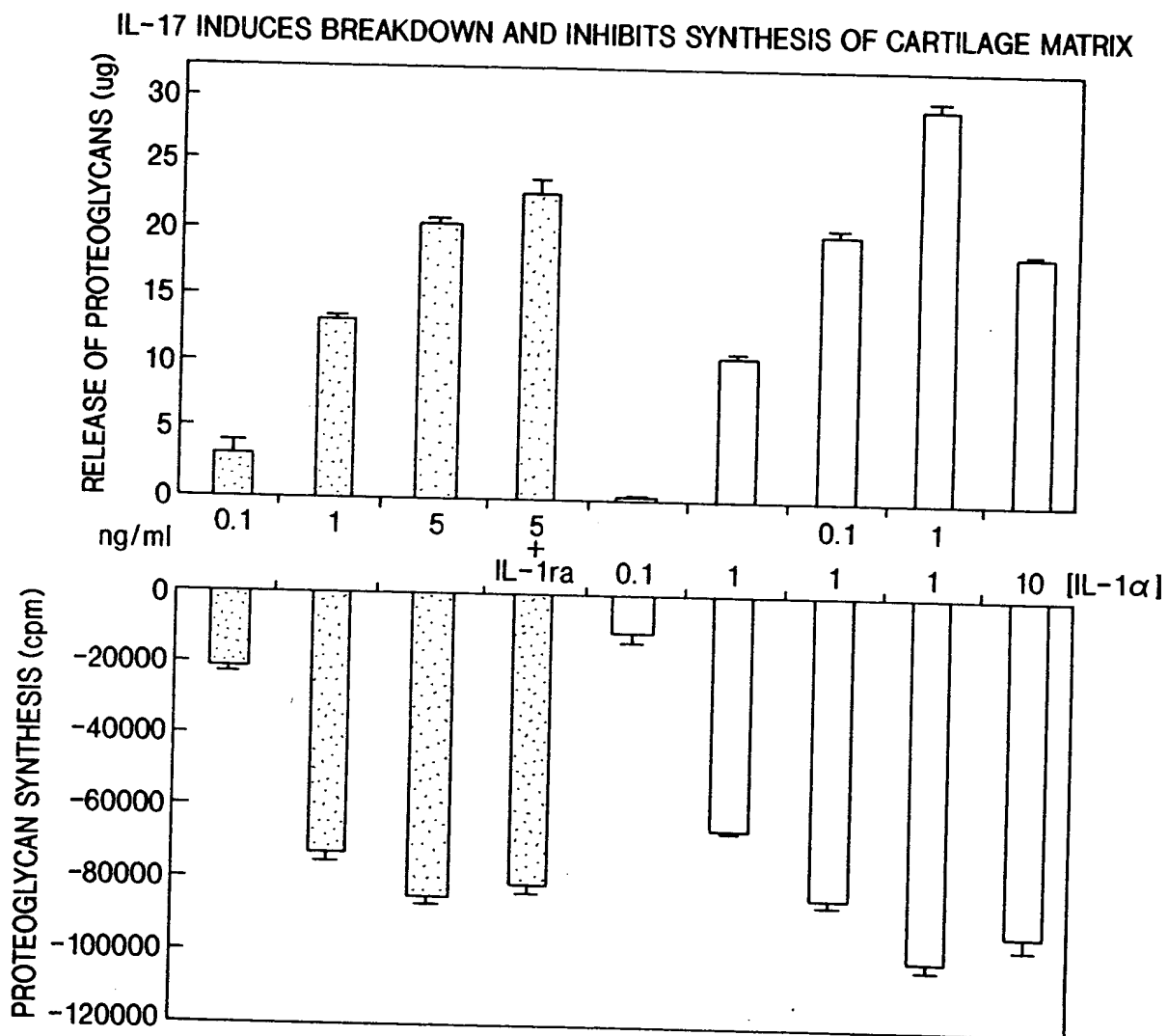


FIG. 39

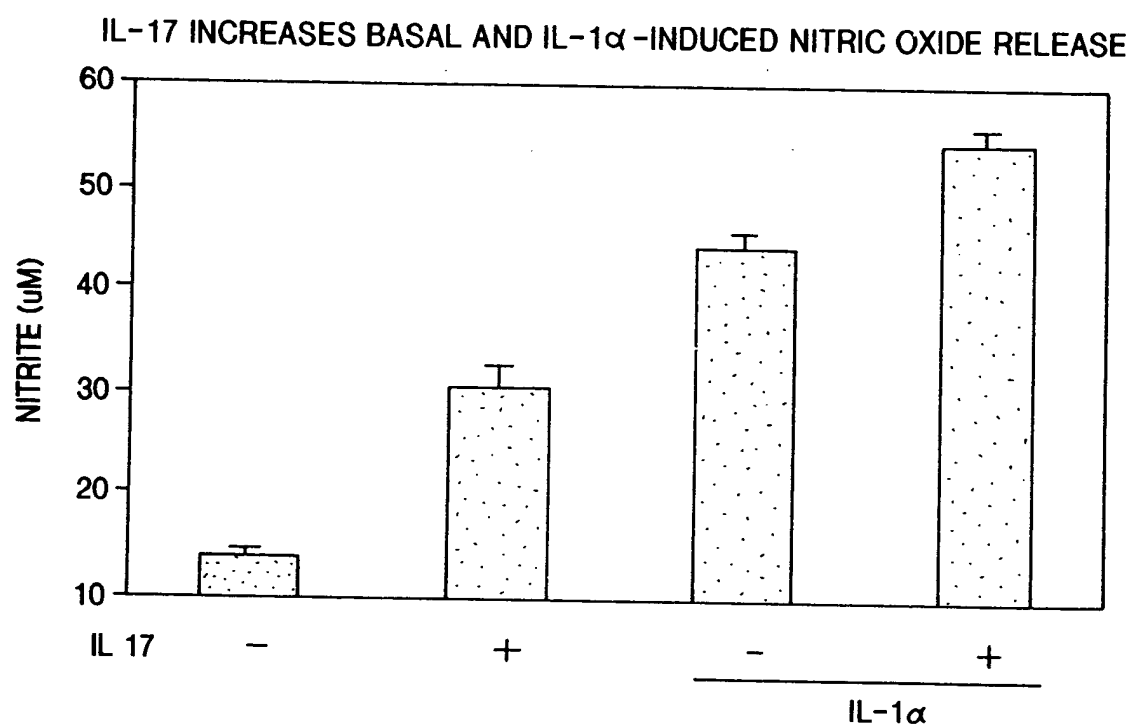


FIG. 40

INHIBITION OF NITRIC OXIDE RELEASE DOES NOT BLOCK THE DETRIMENTAL  
EFFECTS OF IL 17 ON MATRIX BREAKDOWN OR SYNTHESIS

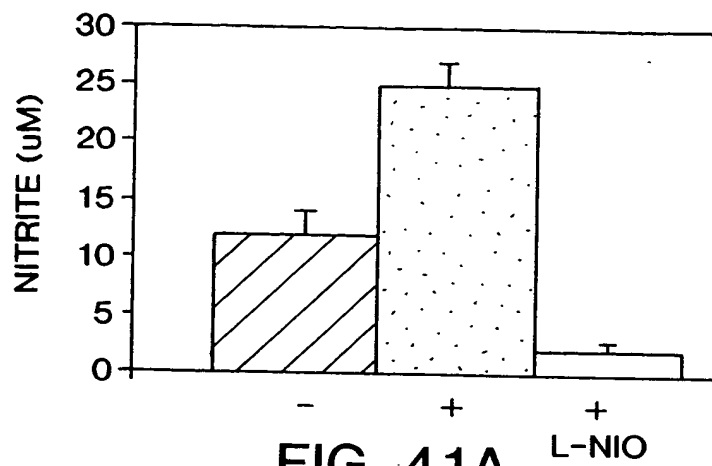


FIG. 41A

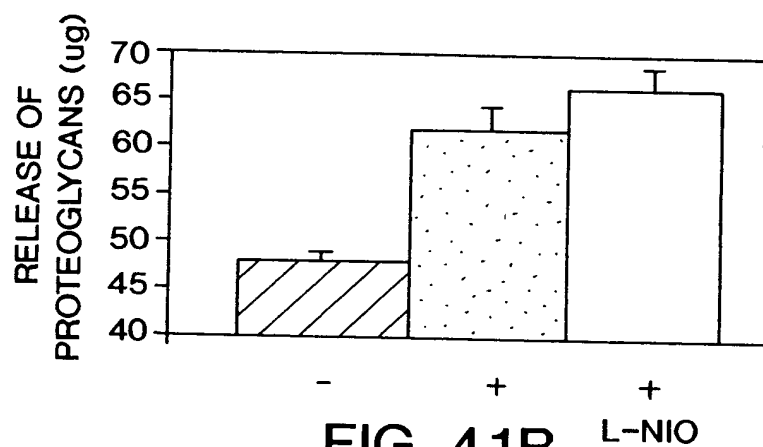


FIG. 41B

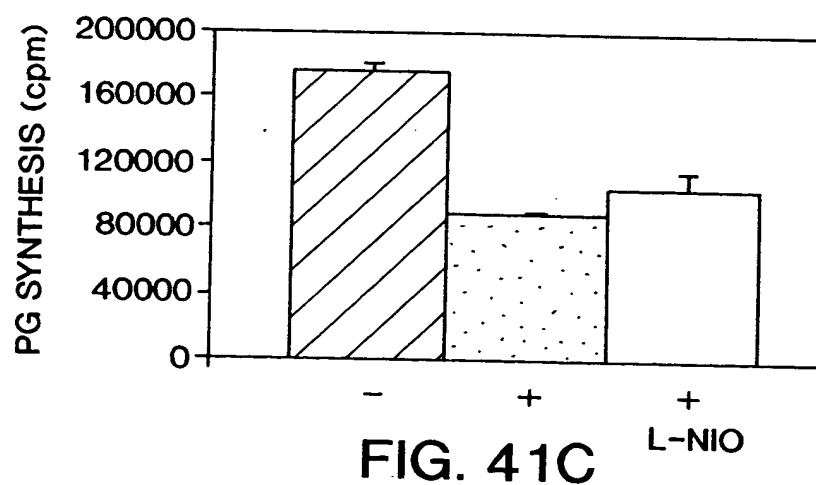


FIG. 41C

INHIBITION OF NO RELEASE ENHANCES IL1- $\alpha$ -INDUCED  
MATRIX BREAKDOWN BUT NOT MATRIX SYNTHESIS

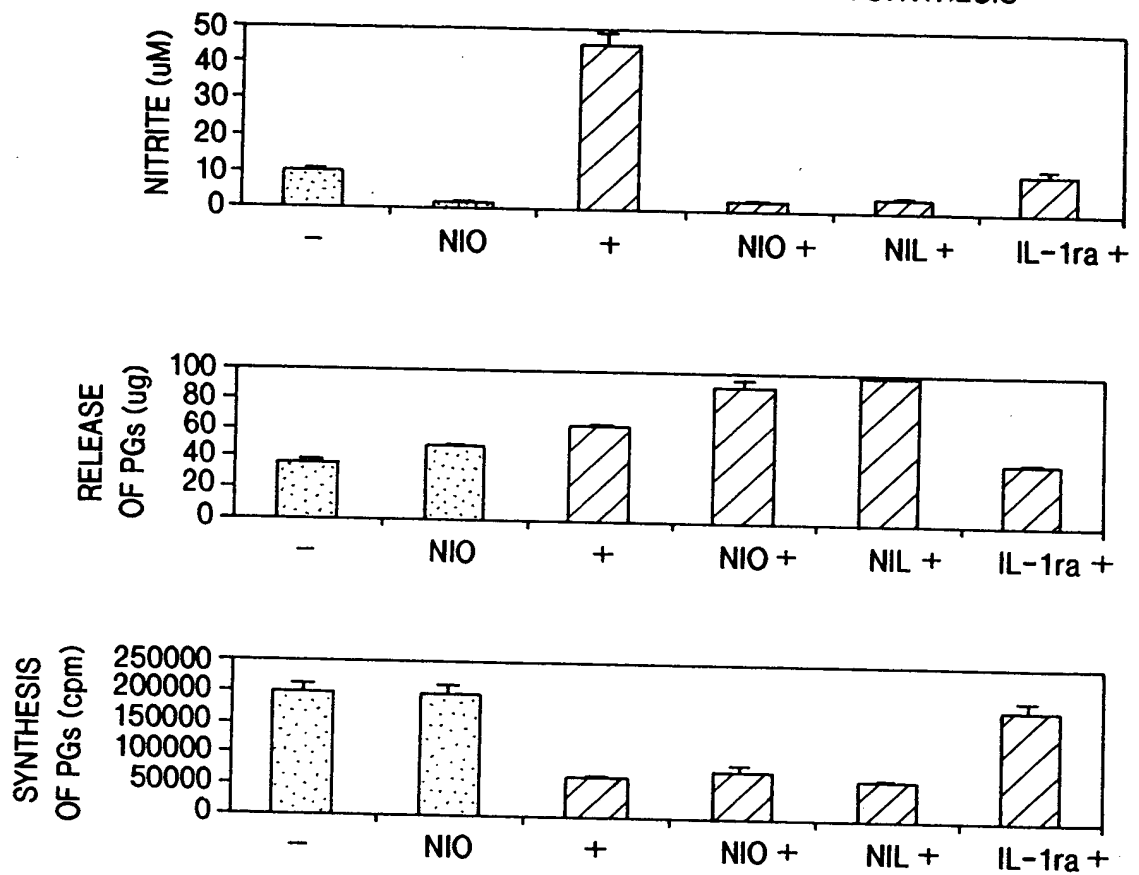


FIG. 42

# IL-17C DETRIMENTAL EFFECTS ON ARTICULAR CARTILAGE

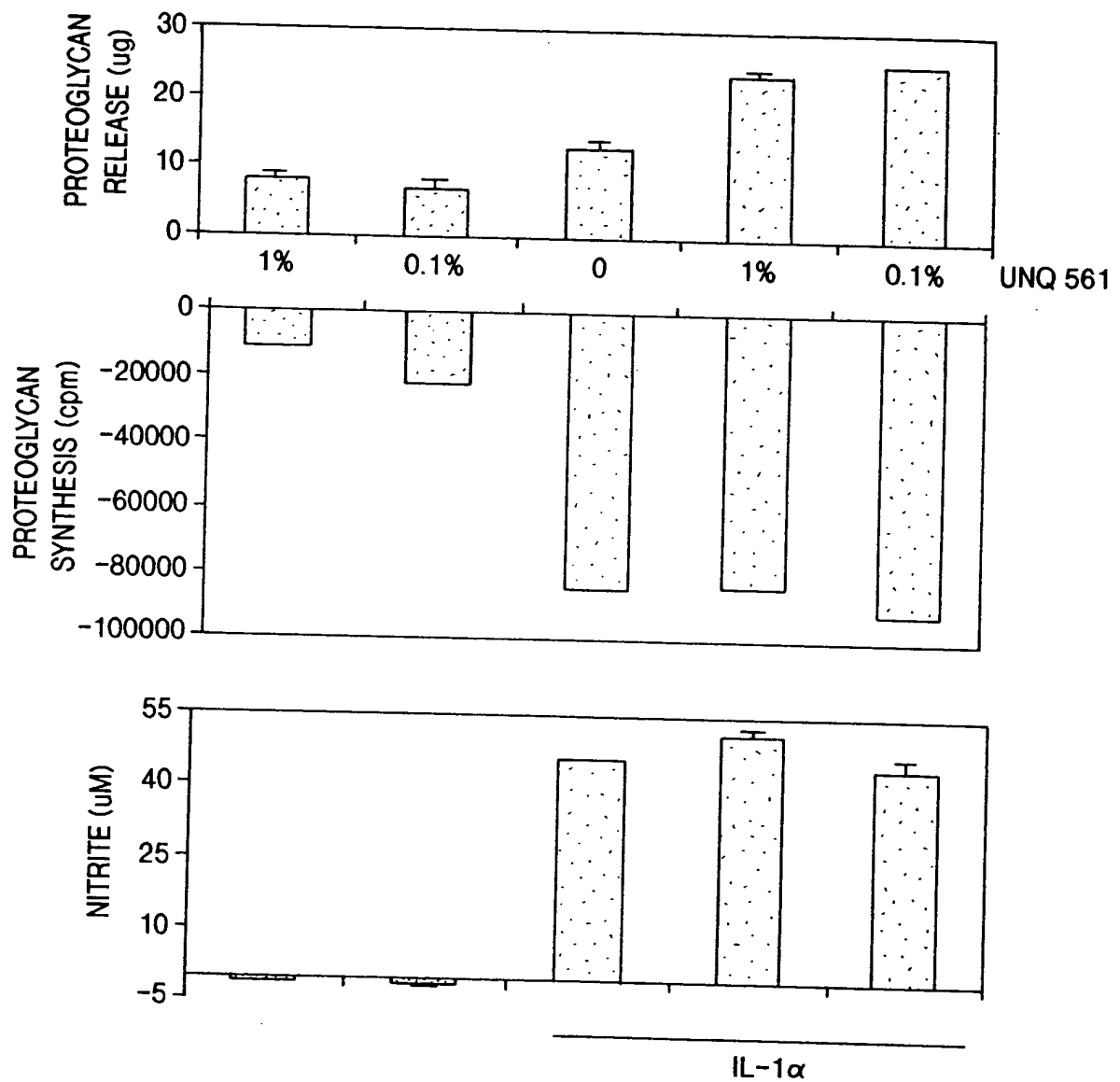


FIG. 43

INFLAMMATORY BOWEL DISEASE:  
EXPRESSION OF IL-17 FAMILY IN MOUSE MODEL OF IBD

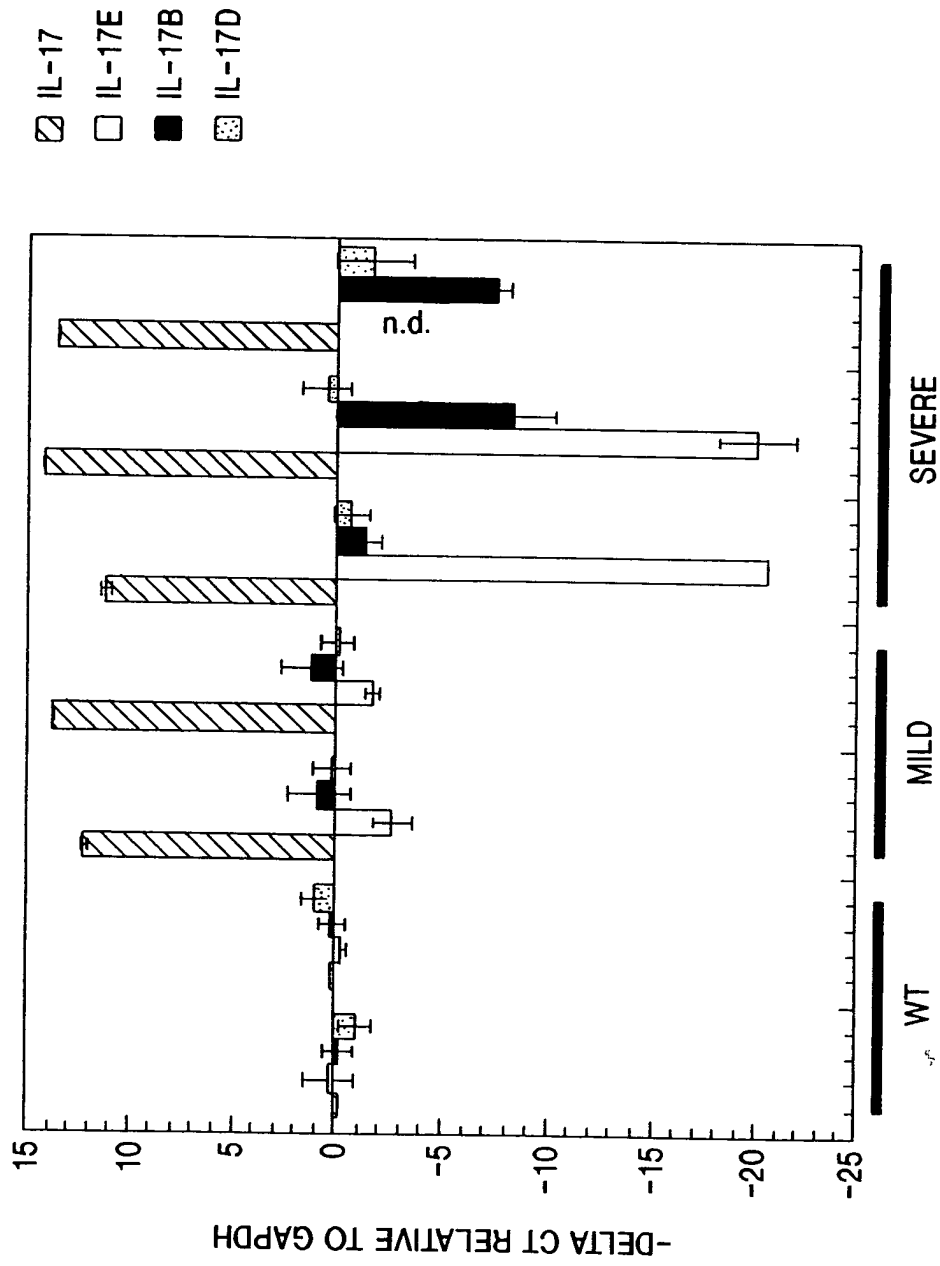


FIG. 44

IL-17D, PRESENT IN BRAIN, DECREASES RAPIDLY FOLLOWING STROKE

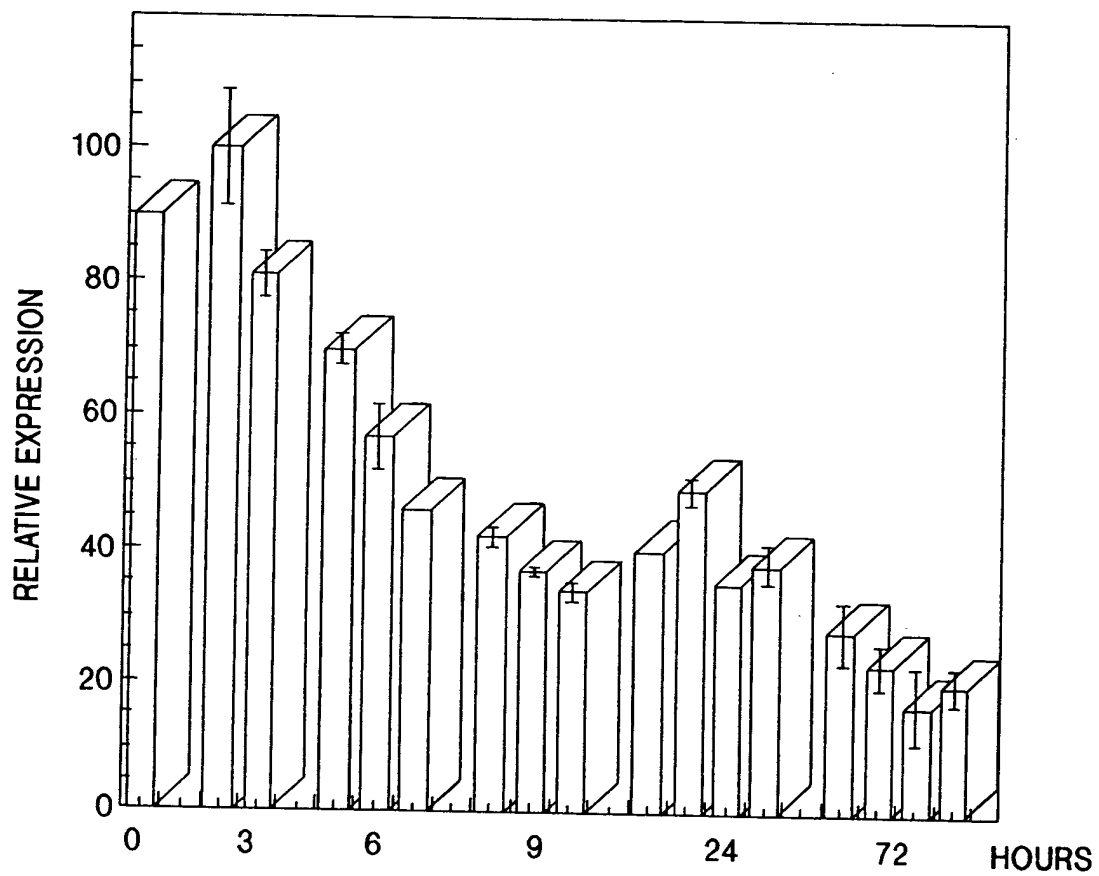
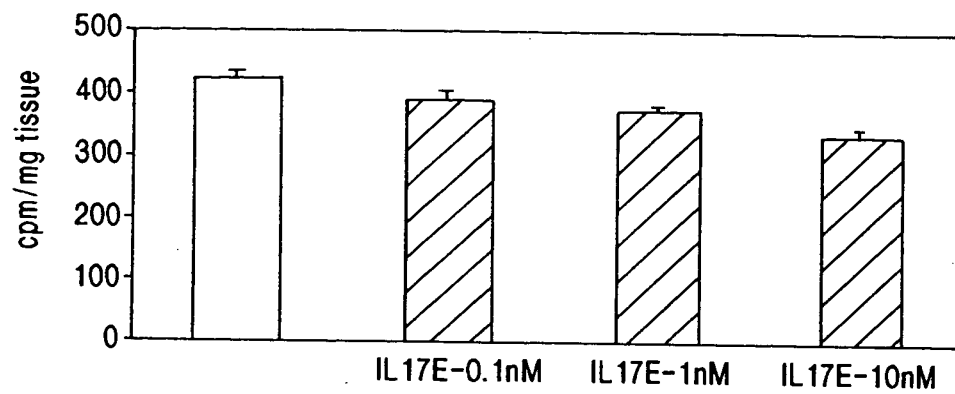
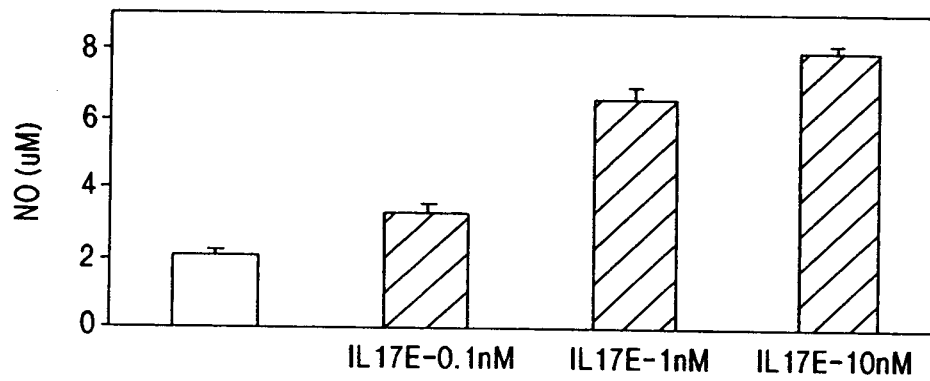


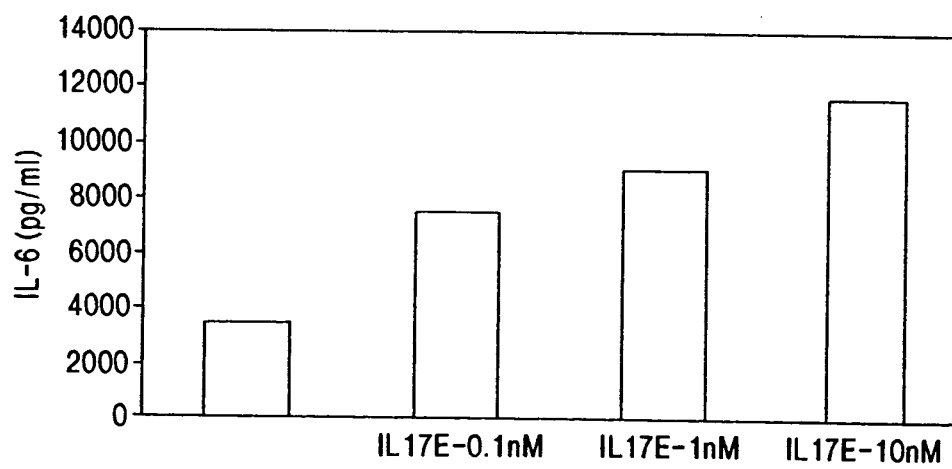
FIG. 45



**FIG. 46A**



**FIG. 46B**



**FIG. 46C**

FIG. 47A

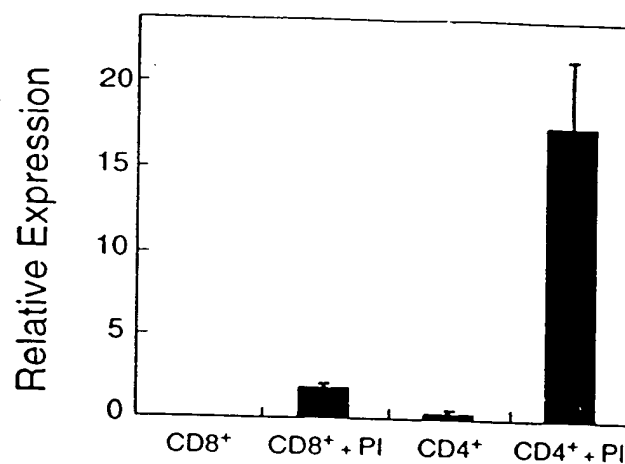


FIG. 47B

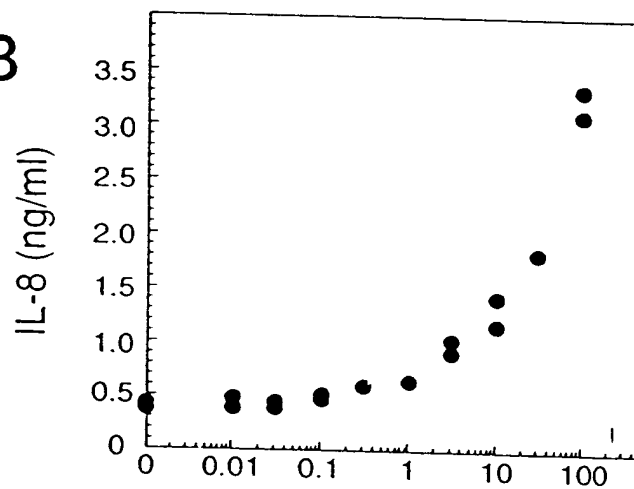
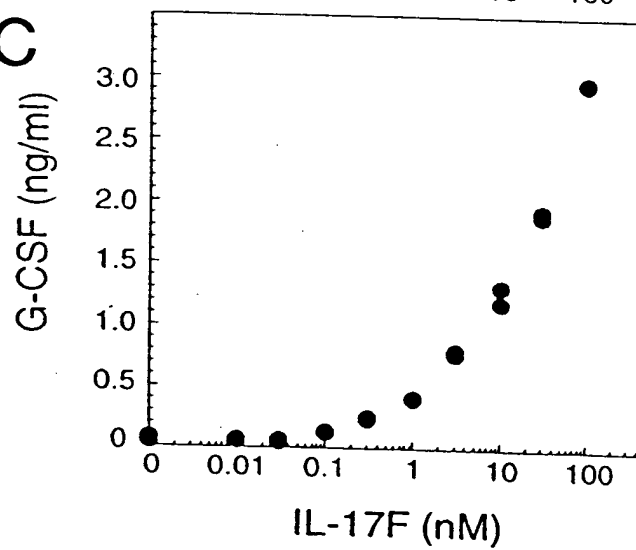
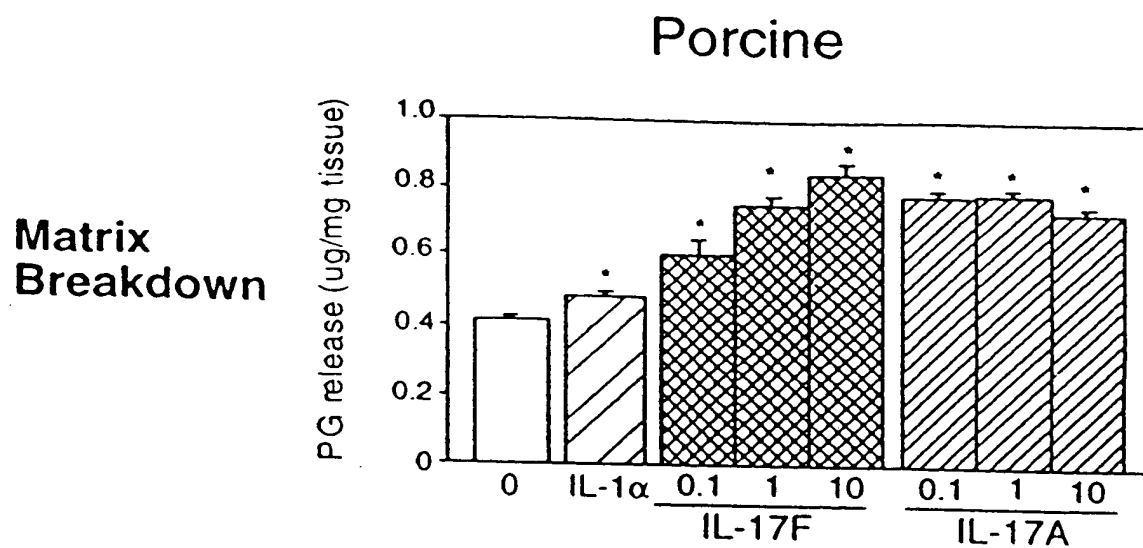
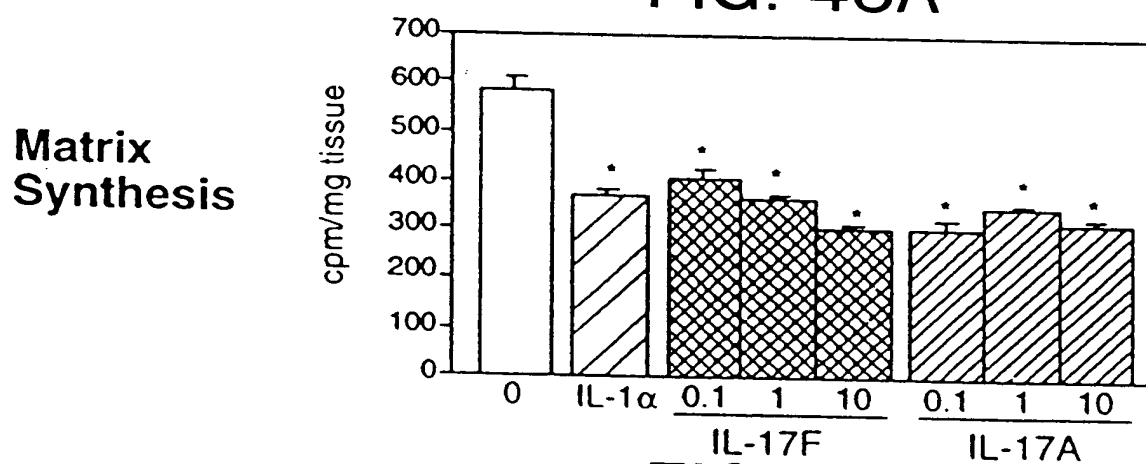


FIG. 47C

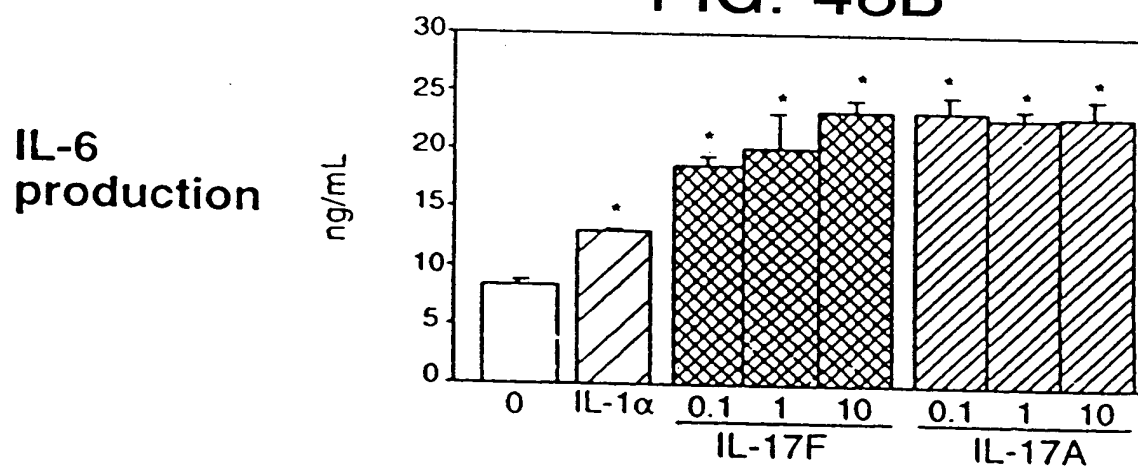




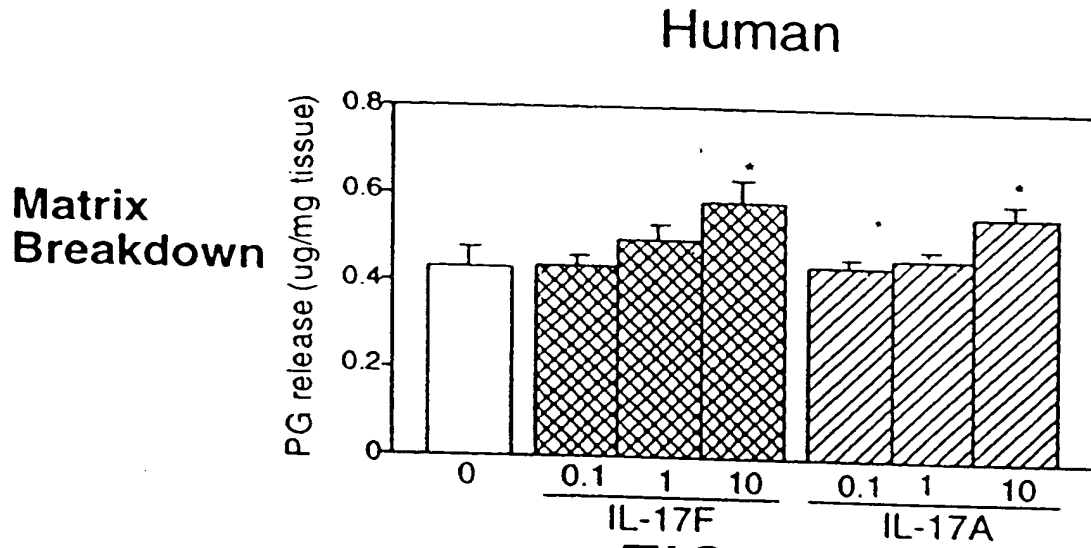
**FIG. 48A**



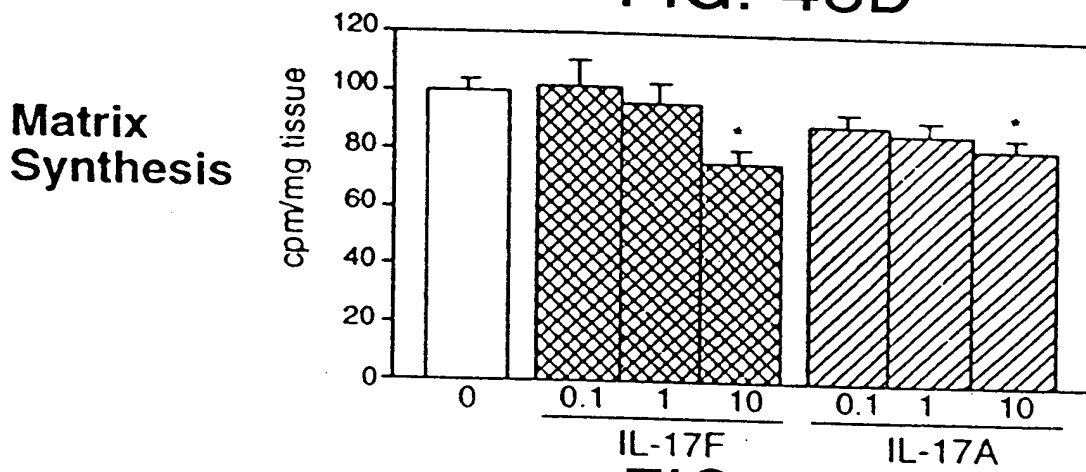
**FIG. 48B**



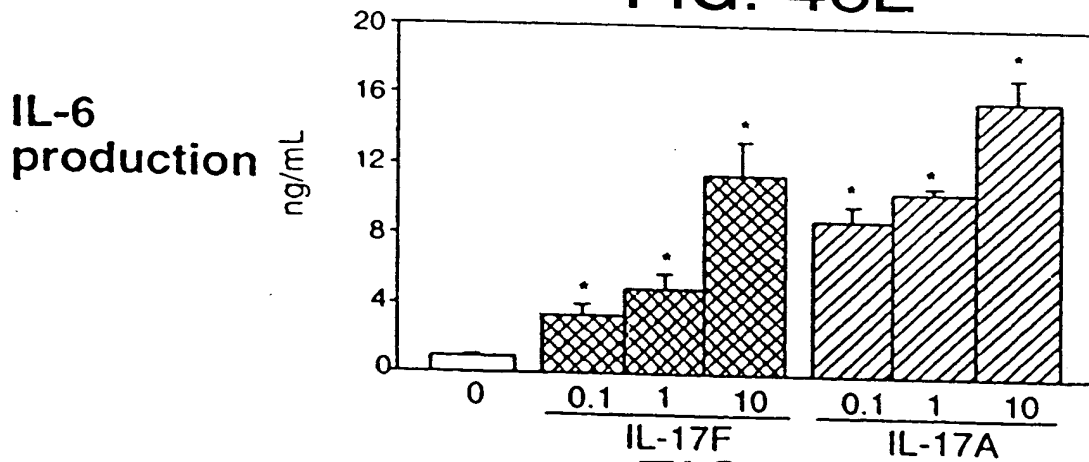
**FIG. 48C**



**FIG. 48D**



**FIG. 48E**



**FIG. 48F**

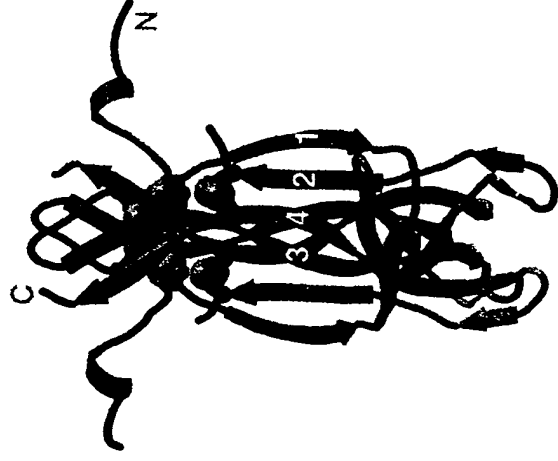
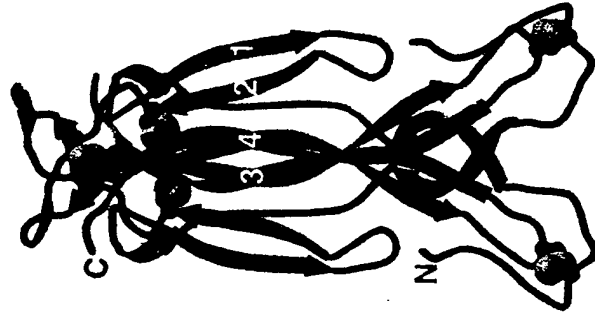
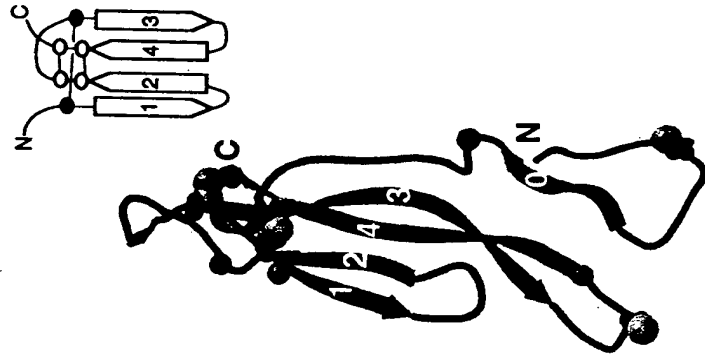


FIG. 49A

FIG. 49B

FIG. 49C

IL-17F	.....	.....	.....	.....	...RKIPKVG	HTFFQKPES	17
IL-17A	.....	.....	.....	.....	...TVKAG	ITIPRNP.G	14
IL-17B	.....QPRS	PKSKRKGQGR	PGPLAPGPHQ	VPLDLVSRMK	PYARMEEYER		44
IL-17C	HHDPSLRGHP	HSHTGTPH.YS	AEELPLGQAP	PHLLARGAKW	GQALPVALVS		50
IL-17E	.....	.....	.....YS	HWPS.PPSKG	QDTSEELLRW		22

IL-17F	PPVPGG....	....SMKLDI	GIINENQRV	MSRNIESRST	PWNYTVTWD	59
IL-17A	PNSDKNFPR	TVMVNLNIHN	RNTNTN..PK	RSDYYNRST	PWNLHNRD	62
IL-17B	NIEEMVAQLR	..NSSELAQR	KCEV....NL	QLWMSNKRSL	PWGYSINHD	88
IL-17C	SLEAASHRGR	..HERPSATT	Q.PVLRPEEV	LEADTHQRSI	PWRYRVDTD	98
IL-17E	STVPVPPLP	..ARPNRHPE	S.RASE....	.DGPLNSRAI	PWRYELDRD	65

IL-17F	PNRYPSEVVQ	AQ.RNLG-IN	A..QGKEDIS	MN VPI.QQE	TLVVRKHKQG	106
IL-17A	PERYPVIWE	AK.RHLG-IN	A..DGNVDYH	MN VPI.QQE	ILVLRREPPH	109
IL-17B	PSRIPVDLPE	AR.LGLG-VN	PF.TMQEDRS	MV.VPV.FSQ	VPVRRR...L	133
IL-17C	EDRYPQKLAF	AE.LCRG-ID	AR.TGRETA	LN VRL.LQS	LLVLR...RP	144
IL-17E	LNRLPQDLYH	AR.LPH-VS	LQTGSHMDPR	GN ELLYHNQ	TVFYRRP... 112	

IL-17F	CSV.....	....SFQLEK	VL..VTUGCT	CMTPIVHHVQ	...	133
IL-17A	CPN.....	....SFRLEK	IL..VSVGCT	CMTPIVHHVA	...	136
IL-17B	CPPPPRTGP.	....CRQRA	VMTIAGCT	CIF.....	...	160
IL-17C	CSRDGSGGLPT	PGAFATHTF	IH..VPVGT	CV.LPRSVAA	ALE	184
IL-17E	CHGEKGTHKG	....YCLER	RLYRVSLACV	CVRPRVMG..	...	145

FIG. 50

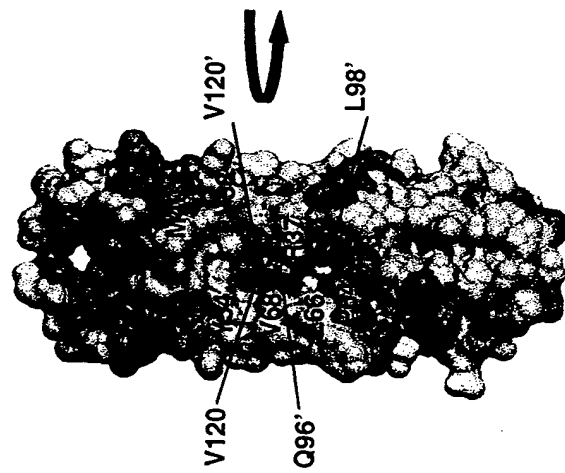


FIG. 51A

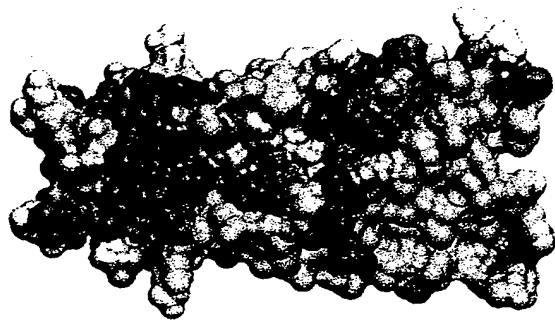


FIG. 51B



FIG. 51C

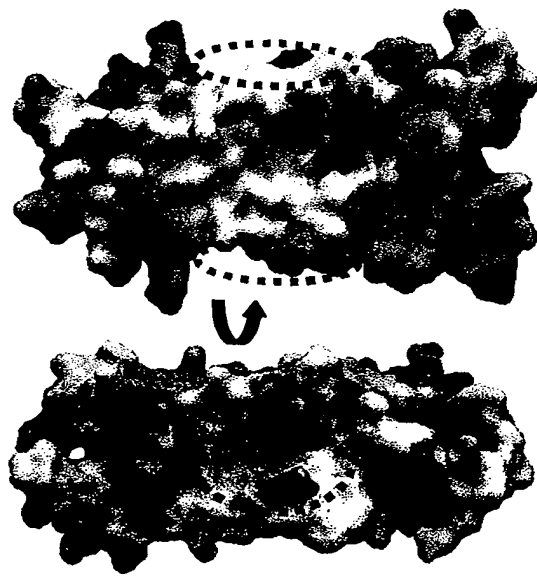


FIG. 52A

FIG. 52B

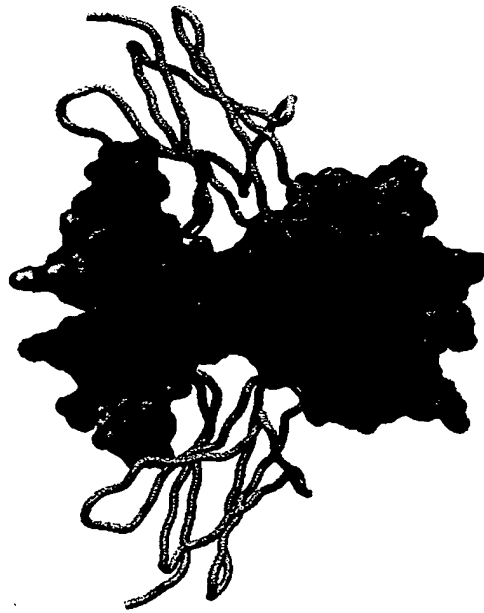


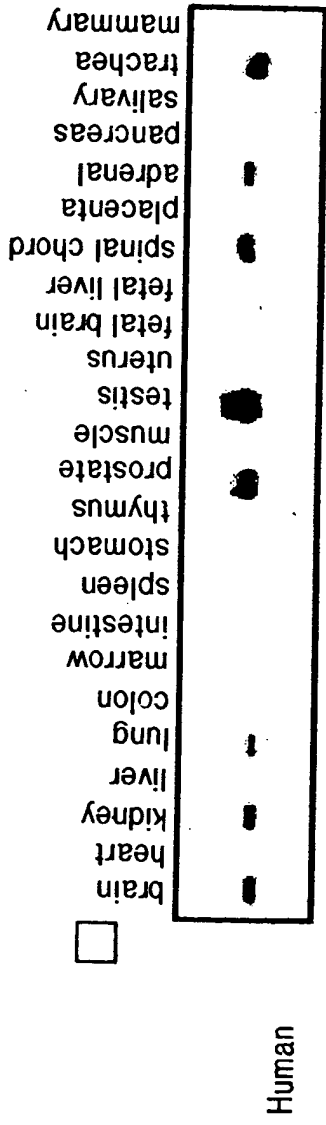
FIG. 52C

IL-17E is highly conserved between human and mouse

mIL-17E	1	-----	VAFLAMIVGTH	TVSLRIQEGC	SHLPSCCPS
hIL-17E	1	MRERPRLGEDSSLISLF	QVVAFLAMVMGTH	-----Y	SHWPSCCPS
mIL-17E	35	KEQEPPEEWLKWSSASVSPPEPLSHTHHAE	ESCRA	SKDG	P
hIL-17E	43	KGQDTSSEELLRLRWS	TVPVPLEP	ARPNRHP	ESCRA
				SE	DG
				P	P
				L	L
				Y	Y
mIL-17E	85	ELDRDLNRVLPQDL	YHARCLCPHCVSLQTGSHMD	PLGNSVP	LYHNQTVFYR
hIL-17E	93	ELDRDLNRVLPQDL	YHARCLCPHCVSLQTGSHMD	PLRGNS	ELLYHNQTVFYR
mIL-17E	135	RPCHGE	EGTHRR	YCLERRLYRVSLACVCVRPR	VMA
hIL-17E	143	RPCHGE	KGTHK	GYCLERRLYRVSLACVCVRPR	VMG

FIG. 53

Tissue distribution of IL-17E



IL-17E (PCR then probed with cDNA)

FIG. 54B

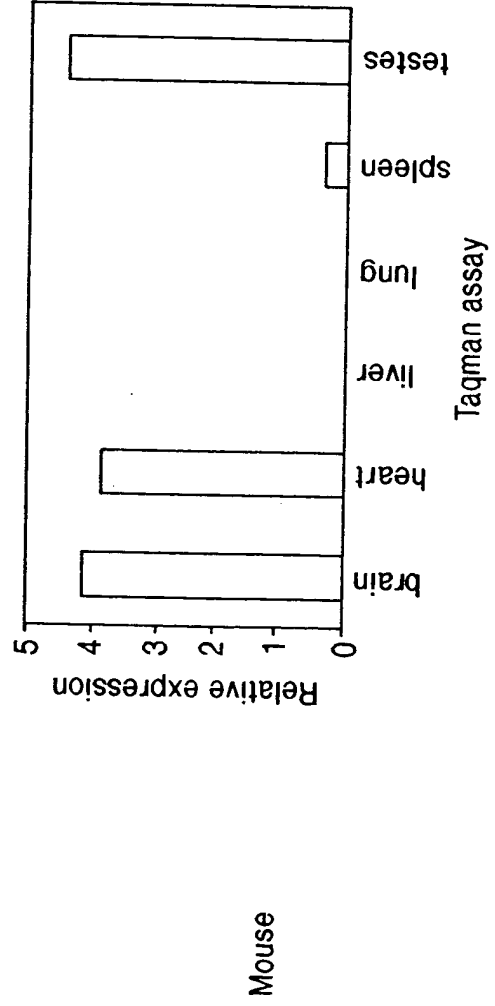


FIG. 54A

mIL-17E transgenics are growth retarded

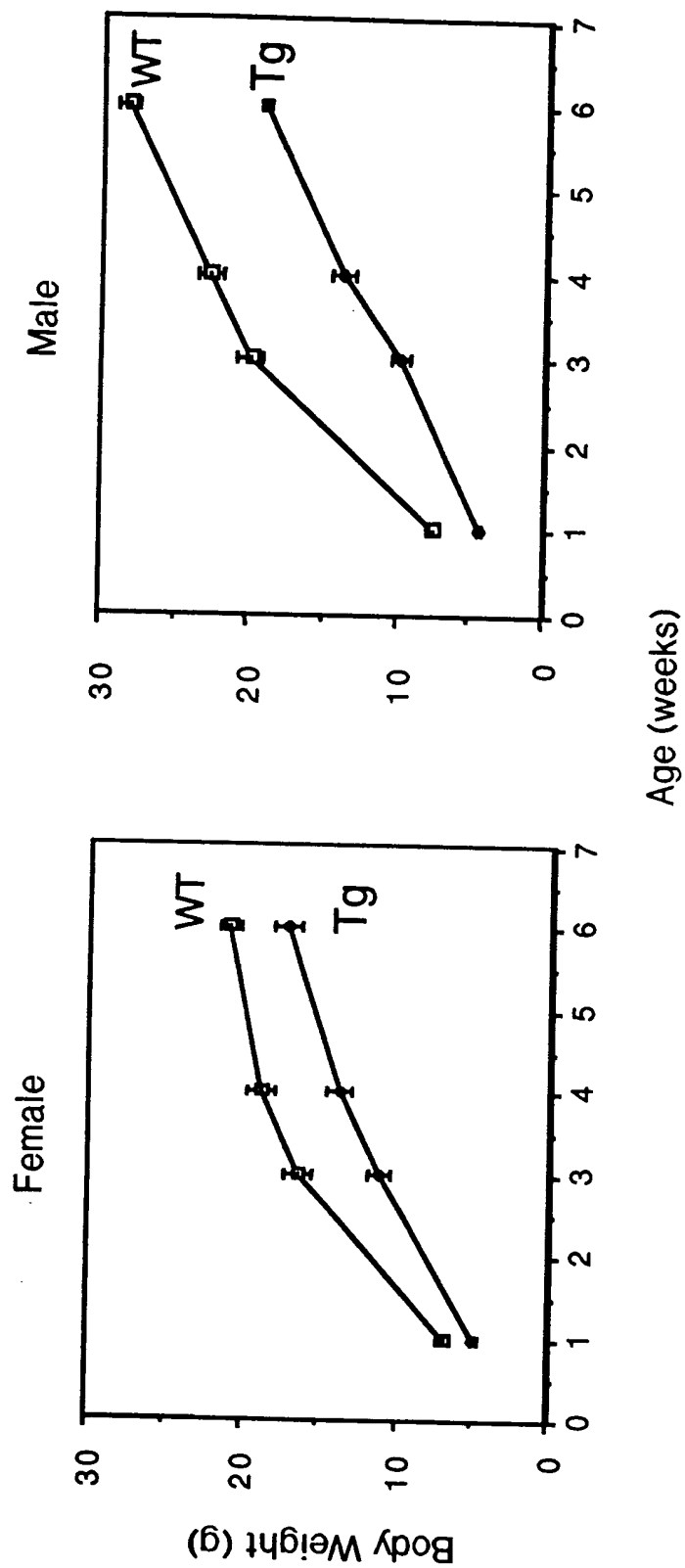


FIG. 55

IL-17E transgenics are jaundiced by 6 weeks of age



FIG. 56

mIL-17E transgenics have elevated total bilirubin and liver enzymes

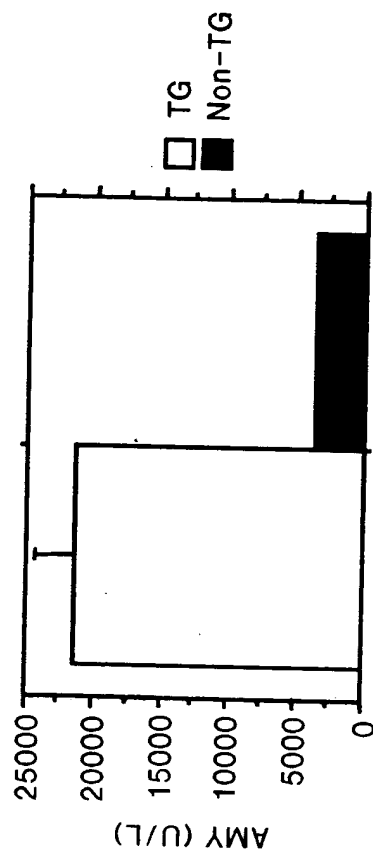
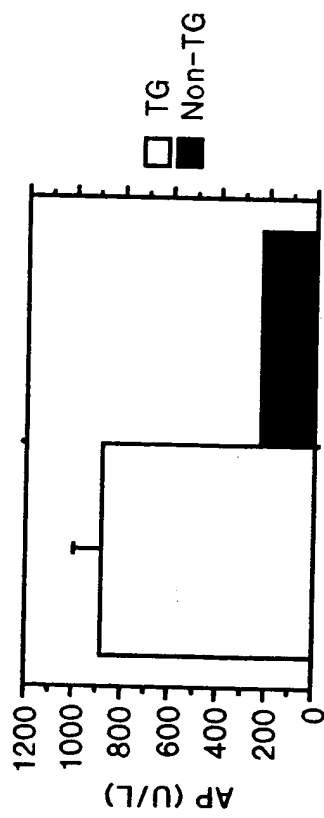
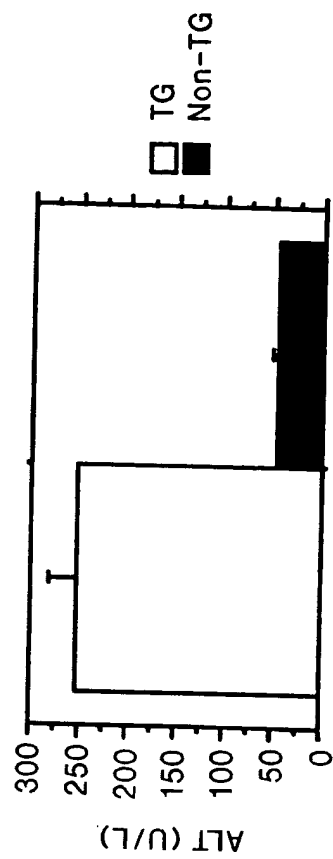
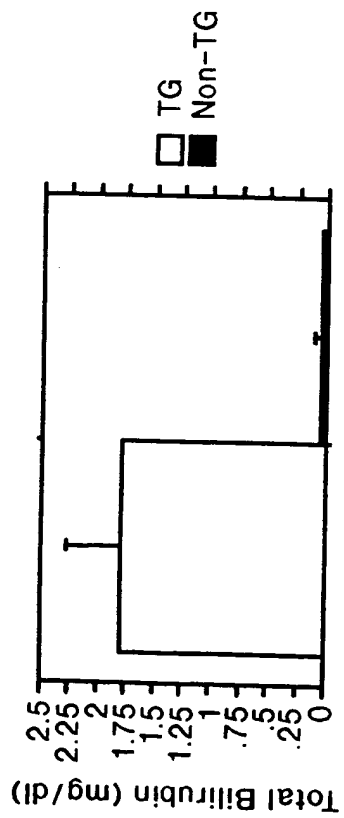


FIG. 57

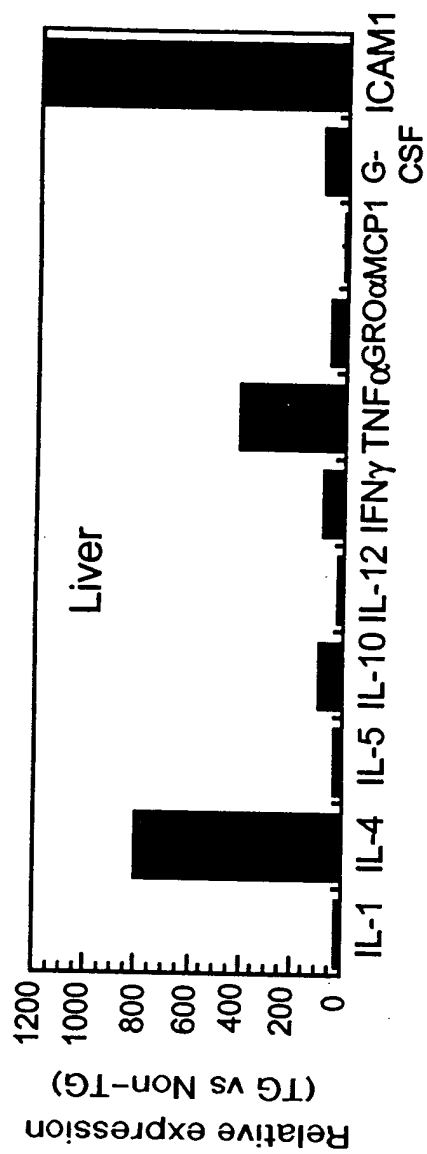


FIG. 58A

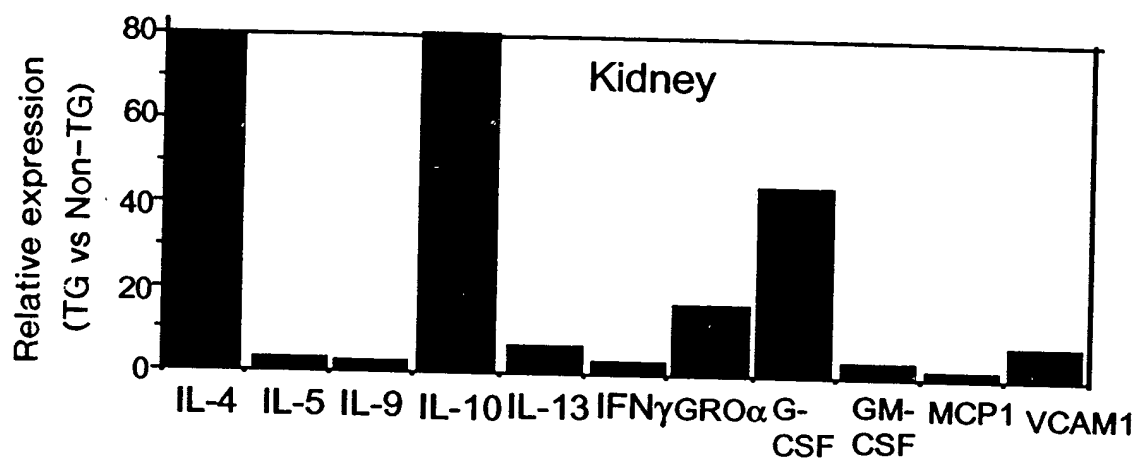


FIG. 58B

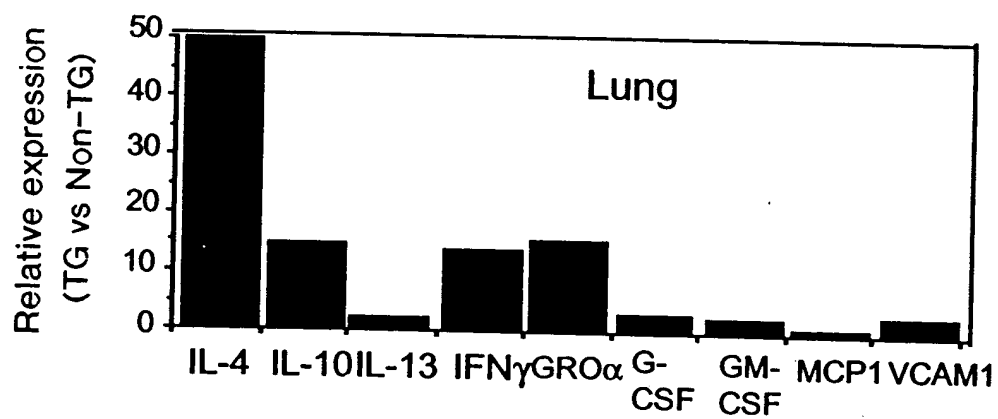
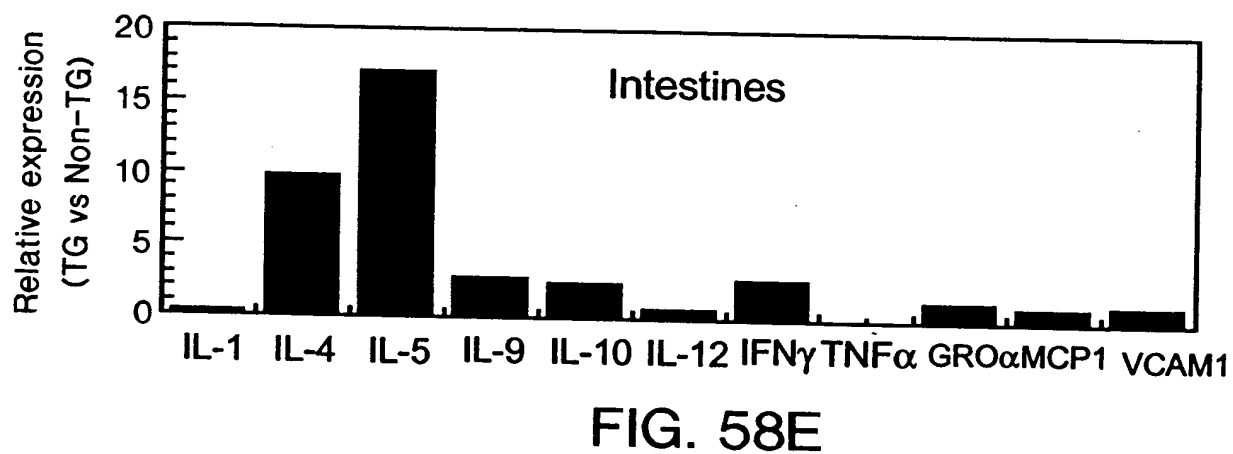
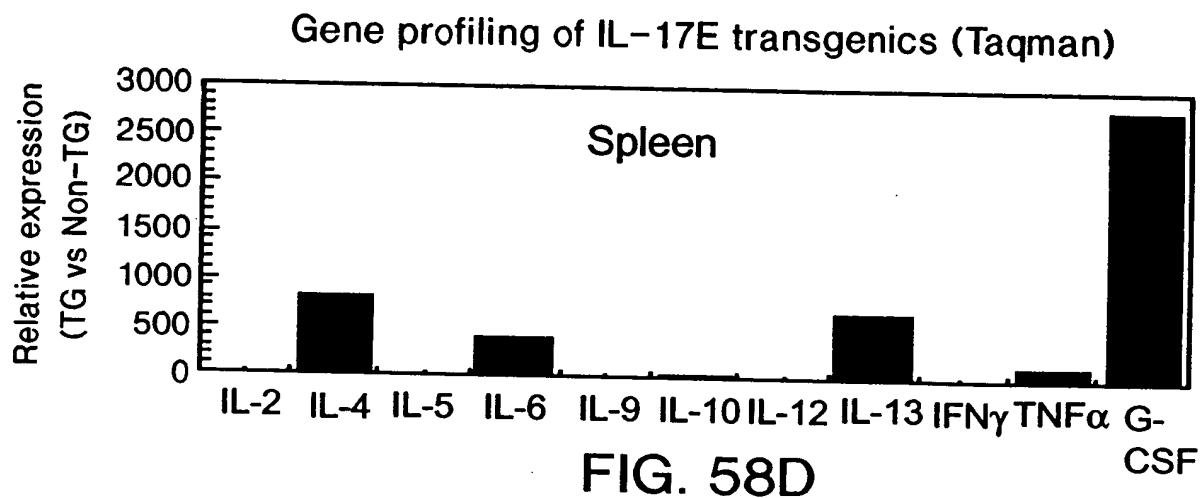


FIG. 58C



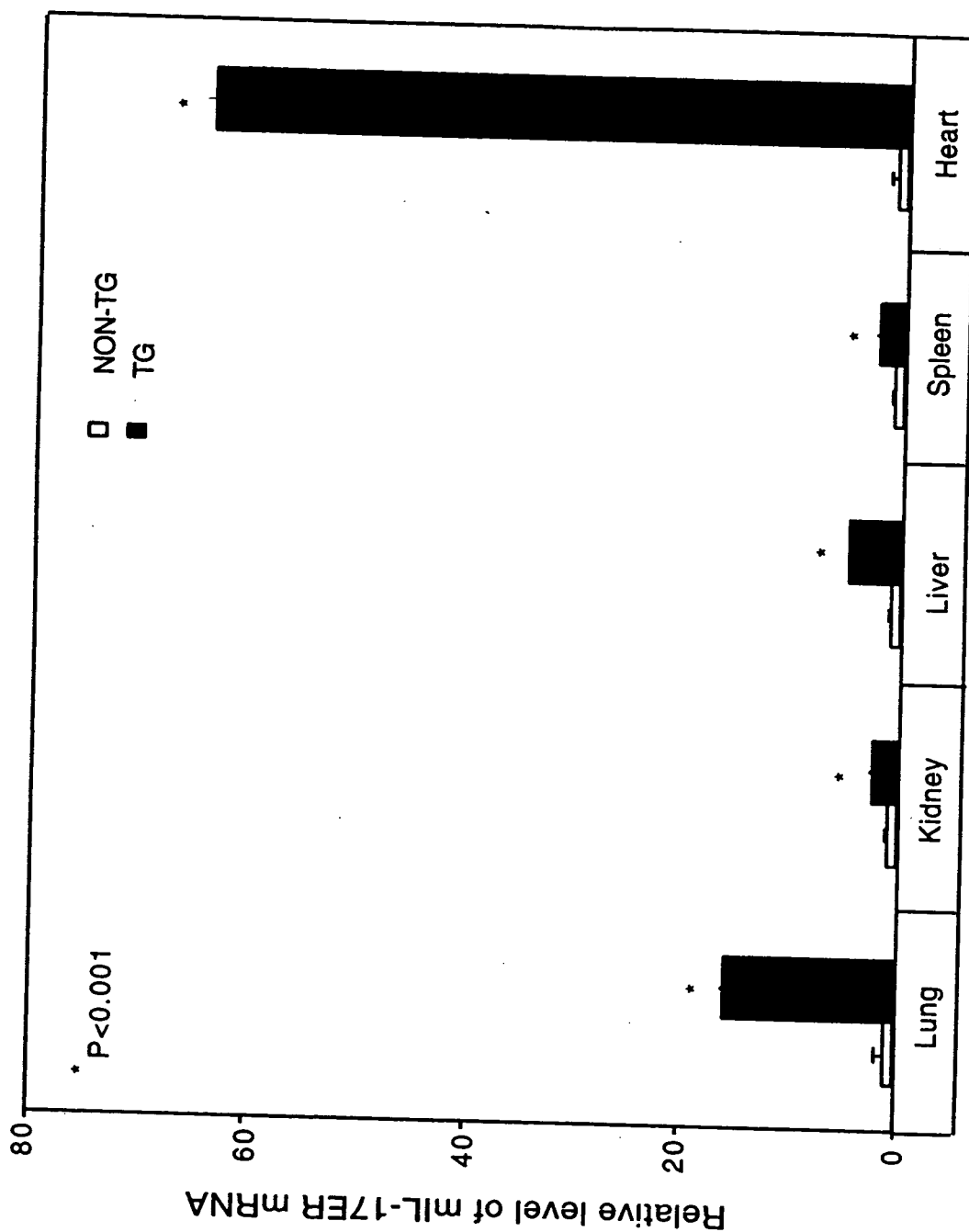


FIG. 59

Elevated serum IL-5, IL-13 and TNF  $\alpha$   
in mIL-17E transgenics

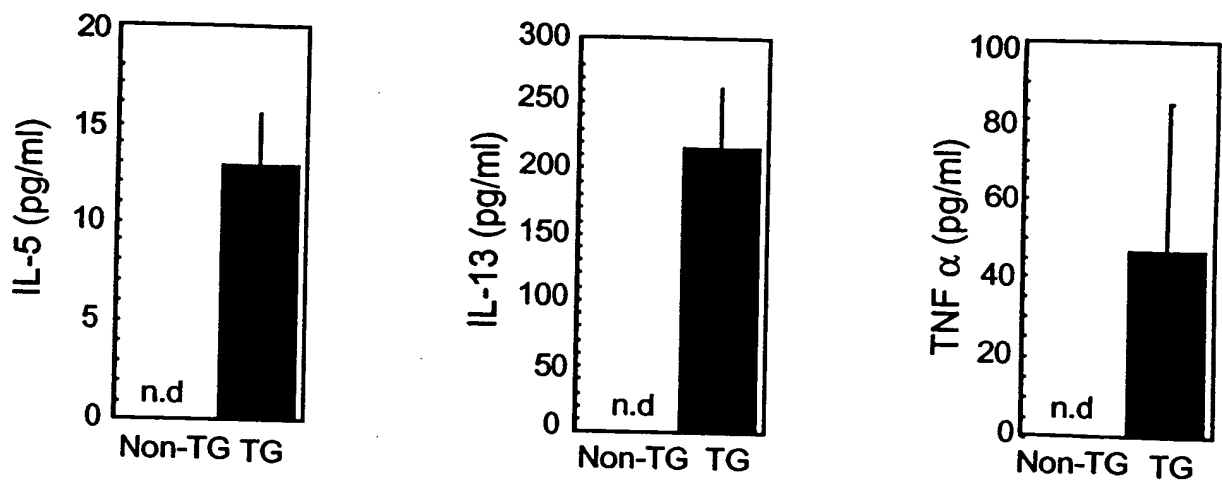


FIG. 60

Serum IgE and IgG 1, but not IgG2a is elevated  
in mL-17E transgenics

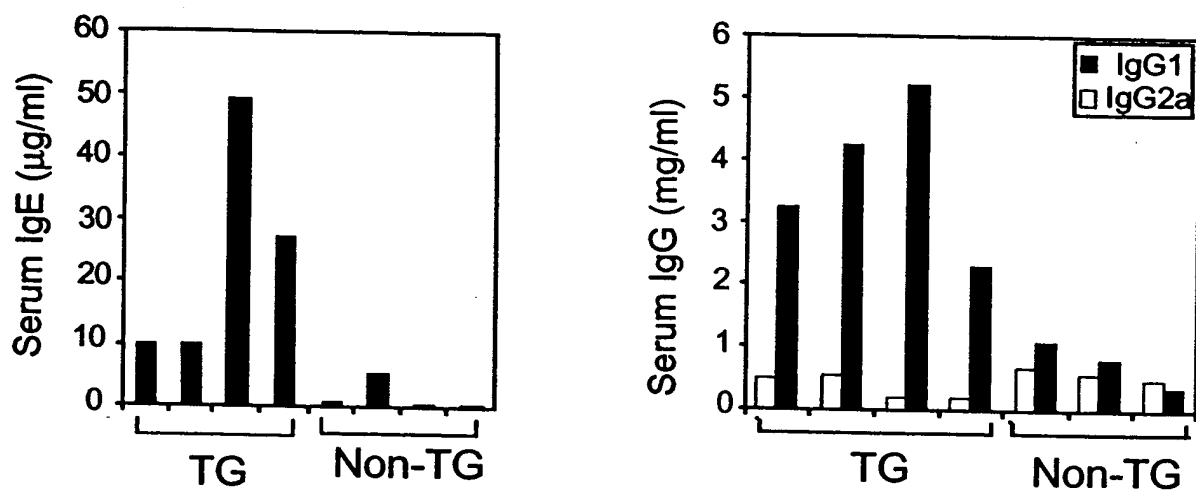


FIG. 61

Neutrophilia in mIL-17E transgenics  
(8 wks, PBMC by FACS)

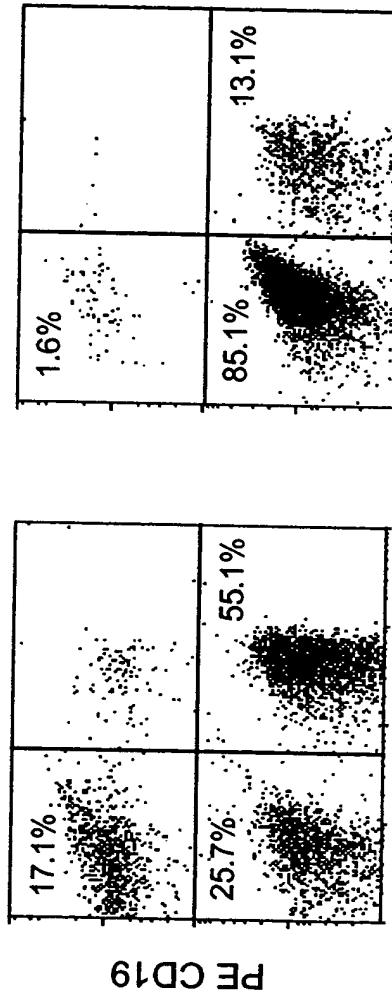


FIG. 62A

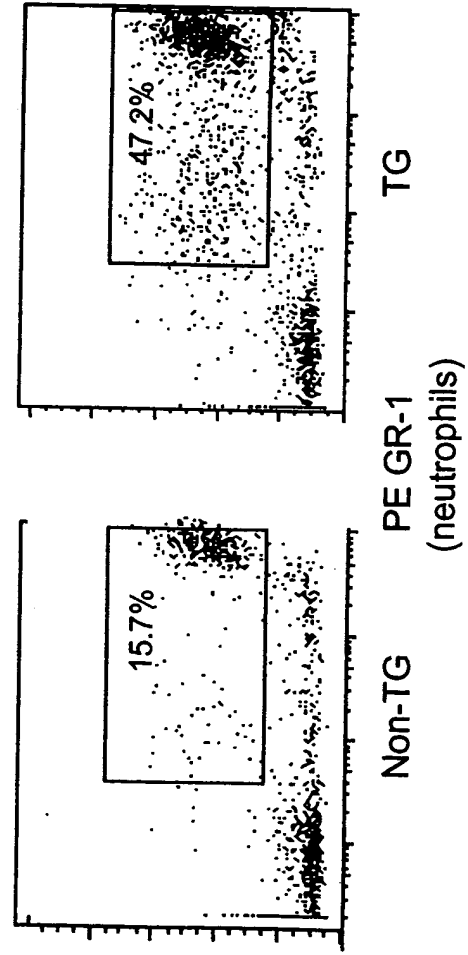


FIG. 62B

Neutrophilia and eosinophilia in mIL-17E transgenics (hematology)

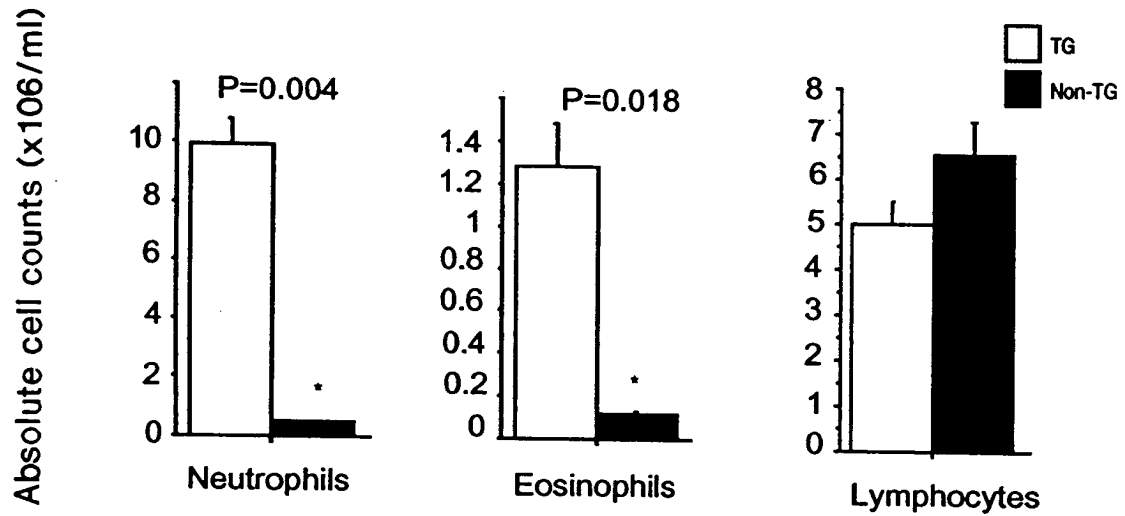


FIG. 63

G-CSF is elevated in  
mIL-17E transgenics

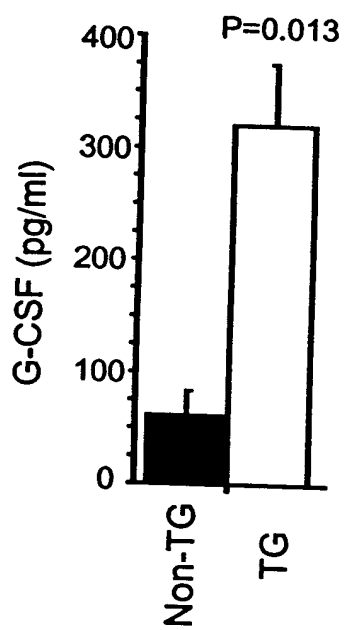
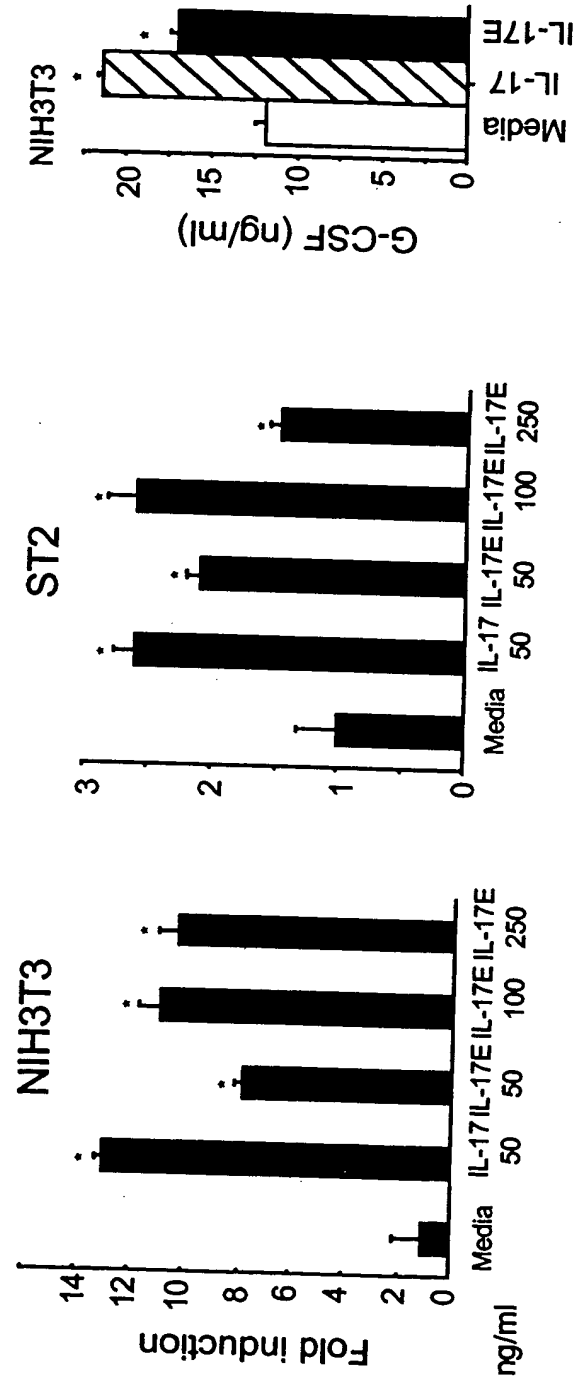


FIG. 64

# IL-17E induces production of G-CSF in vitro



\*P<0.05

FIG. 65

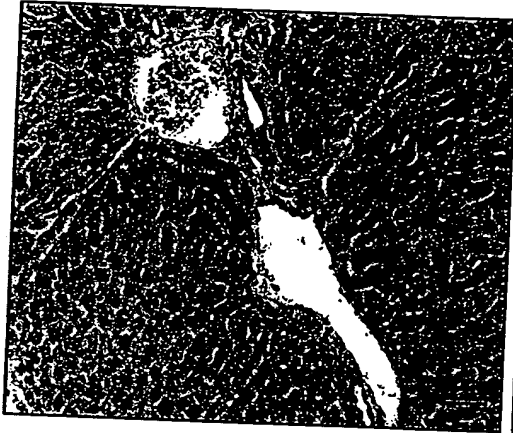


FIG. 66A



FIG. 66B



FIG. 66C

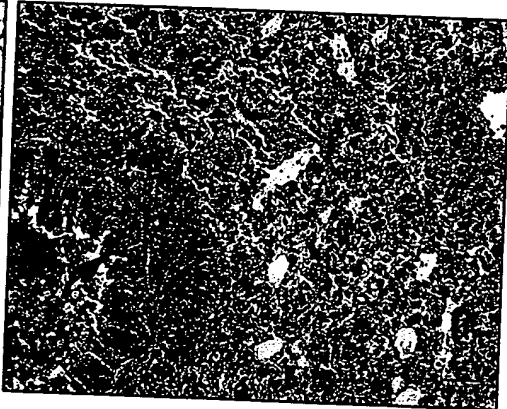


FIG. 66D